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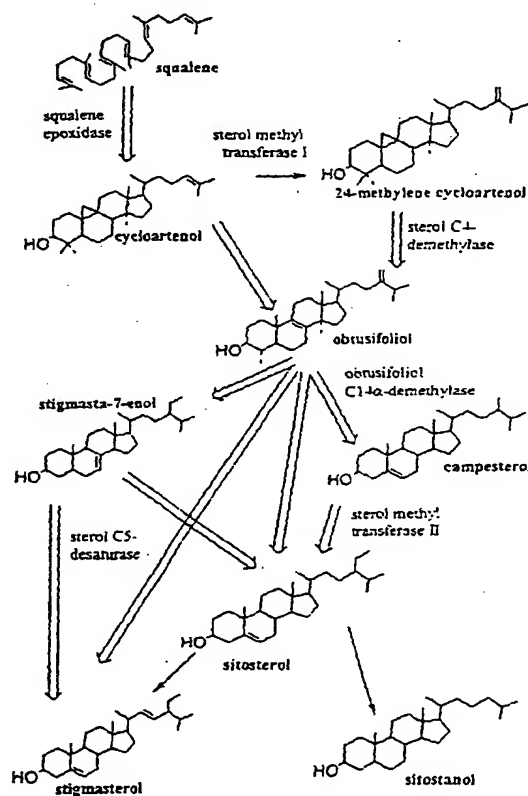
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[Continued on next page]

(54) Title: TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROID COMPOUNDS



(57) Abstract: Disclosed are constructs comprising sequences encoding 3-hydroxy-3methylglutaryl-Coenzyme A reductase and at least one other sterol synthesis pathway enzyme. Also disclosed are methods for using such constructs to alter sterol production and content in cells, plants, seeds and storage organs of plants. Also provided are oils and compositions containing altered sterol levels produced by use of the disclosed constructs. Novel nucleotide sequences useful in the alteration of sterol production are also provided. Also provided are cells, plants, seeds and storage organs of plants comprising sequences encoding 3-hydroxy-3methylglutaryl-Coenzyme A reductase, at least one other sterol synthesis pathway enzyme and at least one tocopherol synthesis enzyme.

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TRANSGENIC PLANTS CONTAINING ALTERED LEVELS
OF STEROID COMPOUNDS

5 TECHNICAL FIELD

 The present invention relates to biotechnology with an emphasis on plant biotechnology, and particularly biotechnology affecting the biosynthesis of steroid compounds.

10

BACKGROUND

 Enhancement of the nutritional or health benefits of oils through genetic engineering is being addressed throughout the agricultural community. Several approaches
15 involve manipulation of already present cellular biosynthetic pathways. Steroid biosynthetic pathways are of current interest, particularly for the enhancement of health benefits from food oils.

 Several related U.S. patents address increasing sterol
20 accumulation in higher plants. Those patents include U.S. Patent No. 5,589,619 "Process and Composition for increasing squalene and sterol accumulation in higher plants" (accumulation of squalene in transgenic plants by increasing HMGR activity) and U.S. Patent No. 5,306,862 "Method and
25 composition for increasing sterol accumulation in higher plants" (increasing HMGR activity to increase plant sterol accumulation--including sterol and cycloartenol, which affects insect resistance--in tobacco, tomato, corn, carrot, soybean, cotton, barley, arabidopsis, guayule and petunia;
30 seeds with elevated sterol/cycloartenol, 7S promoter and CaMV promoters), U.S. Patent No. 5,365,017 "Method and composition for increasing sterol accumulation in higher plants" (DNA construct with HMGR-CaMV 35S, transgenic

plants, hybrid plants, corn, soy, barley, tomato, *Arabidopsis*), U.S. Patent No. 5,349,126 "Process and composition for increasing squalene and sterol accumulation in higher plants" (increase in squalene and sterol
5 accumulation by increasing HMGR activity in transgenic tobacco, cotton, soybean, tomato, alfalfa, *Arabidopsis*, corn, barley, carrot and guayule plants), and EP 486290 (enhancement of squalene and specific sterol [squalene zymosterol, cholest-7,24-dienol, cholest-5,7,24-trienol]
10 accumulation in yeast by increasing HMGR activity in yeast deficient in enzymes that convert squalene to ergosterol).

In those patents, the amount of a protein exhibiting 3-hydroxy-3-methylglutaryl Coenzyme-A reductase (HMGR) activity is typically increased. HMGR widens a "bottleneck"
15 near the beginning of a biosynthetic path to steroid production, permitting a higher carbon flux through steroid biosynthetic pathways and resulting in increased sterol accumulation.

U.S. Patent No. 5,480,805 "Composition for modulating sterols in yeast" (enhancement of delta 8-7 isomerase
20 activity-ERG2 enhances accumulation of specific sterols in yeast).

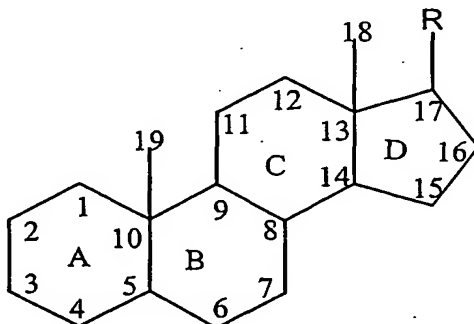
U.S. 5,460,949 "Method and composition for increasing the accumulation of squalene and specific sterols in yeast"
25 (increasing squalene, zymosterol and specific sterols in yeast by increasing HMGR in yeast having decreased *erg5* and *erg6* activity--*Sc* and hamster HMGR).

WO 9845457 (SMTI, *Erg6* from *A.t.*, corn, yeast; transgenic plants with altered sterol levels_using DNA
30 encoding an enzyme binding a first sterol and producing a second sterol--altered carotenoid, tocopherol, modified FA levels--HMGR, 5 α -reductase, geranylgeranyl pyrophosphate synthase, phytoene synthase, phytoene desaturase, isopentenyl diphosphate isomerase).

Acetate is the metabolic precursor of a vast array of compounds vital for cell and organism viability. Acetyl coenzyme A (CoA) reacts with acetoacetyl CoA to form 3-hydroxy-3 methylglutaryl CoA (HMG-CoA). HMG-CoA is reduced to mevalonate in an irreversible reaction catalyzed by the enzyme HMG-CoA reductase. Mevalonate is phosphorylated and decarboxylated to isopentenyl-pyrophosphate (IPP). Through the sequential steps of isomerization, condensation and dehydrogenation, IPP is converted to geranyl pyrophosphate (GPP). GPP combines with IPP to form farnesyl pyrophosphate (FPP), two molecules of which are reductively condensed to form squalene, a 30-carbon precursor of sterols.

A key enzyme in sterol biosynthesis is 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMG-CoA reductase or HMGR). Schaller et al. (Plant Physiol. 109: 761-770, 1995) found that over-expression of rubber HMGR (*hmg1*) genomic DNA in tobacco leads to the overproduction of sterol end-products (sitosterol, campesterol and stigmasterol) up to 6-fold in leaves. Further, the excess sterol was stored as steryl-esters in lipid bodies. HMGR activity was increased by 4- to 8-fold.

Sterols are derivatives of a fused, reduced ring system, cyclopenta-[a]-phenanthrene, comprising three fused cyclohexane rings (A, B, and C) in a phenanthrene arrangement, and a terminal cyclopentane ring (D) having the formula (I) and carbon atom position numbering shown below:



(I)

where R is an 8 to 10 carbon-atom side chain.

In plants, squalene is converted to squalene epoxide, which is then cyclized to form cycloartenol (4,4,14 α -

5 trimethyl-9 β ,19-cyclo-5 α -cholest-24-en-3 β -ol).

Cycloartenol has two methyl groups at position 4, a methyl group at position 14, a methylene bridge between the carbon atoms at positions 9 and 19 that forms a disubstituted cyclopropyl group at those positions, and includes an 8-
10 carbon sidechain of the formula: $\text{CH}_3\text{CH}(\text{CH}_2)_2\text{CH}=\text{C}(\text{CH}_3)_2$.

Squalene epoxide can alternatively be converted into pentacyclic sterols, containing five instead of four rings. Exemplary pentacyclic sterols include the phytoalexins and saponins.

15 Being one of the first sterols in the higher plant biosynthetic pathway, cycloartenol serves as a precursor for the production of numerous other sterols. In normal plants, cycloartenol is converted to predominantly 24-methylene cycloartenol (4,4,14 α -dimethyl-9 β ,19-cyclo-22,23-dihydro-
20 ergosta-24(28)-en-3 β -ol), cycloeucalenol, (4,14 α -trimethyl-9 β ,19 cyclo-5 α -ergosta-24(28)-en-3 β -ol), isofucosterol (5 α -stigmasta-5-24(28)-dien-3 β -ol), sitosterol (5 α -stigmasta-5-en-3 β -ol), stigmasterol-(stigmasta-5,-22-dien-3 β -ol), campesterol (5 α -ergosta-5-en-3 β -ol), and cholesterol (5 α -
25 cholesta-5-en-3 β -ol). These transformations are illustrated in Fig. 1.

Although sterols produced by plants, and particularly higher (vascular) plants, can be grouped by the presence or absence of one or more of several functionalities, plant
30 sterols are classified into two general groups herein; i.e., those containing a double bond between the carbon atoms at positions 5 and 6 (Δ^5 or Δ^5 sterols) and those not

containing a double bond between the carbon atoms at positions 5 and 6 (non-delta-5 sterols).

Exemplary naturally-occurring delta-5 plant sterols are isofucosterol, sitosterol, stigmasterol, campesterol, 5 cholesterol, and dihydrobrassicasterol. Exemplary naturally occurring non-delta-5 plant sterols are cycloartenol, 24-methylene cycloartenol, cycloeucalenol, and obtusifoliol. The most abundant sterols of vascular plants are campesterol, sitosterol, and stigmasterol, all of which 10 contain a double bond between the carbon atoms at positions 5 and 6 are classified as delta-5 sterols.

The HMG-CoA reductase enzymes of animals and yeasts are integral membrane glycoproteins of the endoplasmic reticulum. The intact enzyme comprises three regions: a 15 catalytic region containing the active site of the enzyme; a membrane binding region anchoring the enzyme to the endoplasmic reticulum; and a linker region joining the catalytic and membrane binding regions of the enzymes. The membrane binding region occupies the amino-terminal (N- 20 terminal) portion of the intact protein, whereas the catalytic region occupies the carboxy-terminal (C-terminal) portion of the protein, with the linker region constituting the remaining portion. M.E. Basson et al., *Mol. Cell Biol.*, 8(9):3797-3808 (1988).

25 The activity of HMG-CoA reductase in animals and yeasts is known to be subject to feedback inhibition by sterols. Such feedback inhibition requires the presence of the membrane binding region of the enzyme. See, e.g., G. Gil et al, *Cell*, 41:249-258 (1985); M. Bard and J.F. Downing, *J. 30 Gen. Microbiol.*, 124:415-420 (1981).

Given that mevalonate is the precursor for sterols and other isoprenoids, it might be expected that increases in the amount or activity of HMG-CoA reductase would lead to

increases in the accumulation of both sterols and other isoprenoids.

In mutant strains of the yeast *Saccharomyces cerevisiae* (S. cerevisiae) having abnormally high levels of HMG-CoA reductase activity, the production of two sterols, 4,14-dimethylzymosterol and 14-methylfucosterol is markedly increased above normal. Downing, et al., *Biochem. Biophys. Res. Comm.*, 94(3): 874-979 (1980).

When HMG-CoA reductase activity was increased by illumination in non-photosynthetic microorganisms, isoprenoid (carotenoid), but not sterol (ergosterol), synthesis was enhanced. Tada, et al., *Plant and Cell Physiology*, 23(4):615-621 (1982).

WO 9703202 discloses a method for identifying agents modulating sterol biosynthesis using a yeast acetoacetyl CoA thiolase (ERG10) gene linked to a reporter system to evaluate compounds, such as lovastatin and other HMG-CoA synthase inhibitors, that affect cholesterol biosynthesis.

U.S. Patent No. 5,668,001 teaches a recombinant avian HMG-CoA synthase preparation useful for evaluating drugs that inhibit cholesterol biosynthesis.

JP 09121863 discloses a plant with increased 3-hydroxy-3-methyl glutaryl coenzyme A reductase (HMGR) activity as a result of increasing the expression of a mutant protein kinase gene that regulates expression of the HMGR gene. The increased HMGR activity increases squalene, zymosterol, cholesta-7,24-dienol and cholest-5,7,24-trenol accumulation in yeast with ERG5 and ERG6 mutants.

EP 480730 "Plant-sterol accumulation and pest resistance-by increasing copy number of 3-hydroxy-3-methyl glutaryl coenzyme-A reductase gene in tobacco, tomato and corn

WO 9913086 "Human Delta 7-sterol reductase polypeptide-useful for diagnosis or treatment of genetic defects e.g.

hereditary Smith-Lemli-Opitz syndrome" teaches making and using the recombinant polypeptide with humans.

Chappell et al. U.S. Patent No. 5,589,619 teaches that transformation of higher plants with truncated HMG-CoA reductase enhanced the production of squalene, cycloartenol and certain sterols, particularly compounds having unsaturations at the 5-position. Several intermediate sterols as are shown in Fig. 1 were also produced. It would be beneficial if the production of sitosterol and stigmasterol could be enhanced while lessening the accumulation of the intermediate sterols. The present invention provides avenues for enhancing production of sitosterol and stigmasterol and lessening the accumulation of the intermediate sterols.

Gonzalez et al. (Abstract of poster at Third Terpnet Meeting of the European Network on Plant Isoprenoids, May 29-30, 1997, Poitiers, France) over-expressed the *Arabidopsis* HMGR cDNA (*hmg1* and *hmg2*) and found sterol overproduction with *hmg1* only. They used two forms of the *hmg1* gene, a full-length form and a truncated form containing only the catalytic domain. HMGRs have three domains, an N-terminal membrane spanning domain, a short linker domain, and a C-terminal catalytic domain. In this case the transgenic plants were also *Arabidopsis*. The difference between the full-length and truncated forms was a greater accumulation of pathway intermediates in the case of the truncated form. More importantly, the intermediates demonstrated as accumulating were cycloartenol, 24-methylenecycloartanol and obtusifoliol.

Finally, US patents 5,365,017 and 5,306,862, both assigned to Amoco Corp., disclose a method for increasing sterol accumulation in plants by increasing the copy number of a gene having HMG-CoA reductase activity. These inventions disclose a method using hamster truncated HMGR

that consisted of the catalytic domain and the linker domain. According to the claims the linker domain was essential for activity. They also demonstrated a greater accumulation of pathway intermediates such as cycloartenol.

5

BRIEF SUMMARY

The present invention relates to transgenic plants and their progeny having improved nutritional characteristics. More particularly, the present invention relates to

10 transgenic plants and their progeny, the storage organs (e.g. seed, fruit and vegetable parts) of which contain modified levels of steroid compounds, such as (i) elevated levels of beneficial phytosterols (e.g., sitosterol), phytostanols (e.g., sitostanol), and esters thereof,

15 relative to an otherwise identical plant transformed only with a truncated HMG-CoA reductase gene or a wild-type plant, and (ii) reduced levels of steroid pathway intermediate compounds (e.g. one or more of squalene, cycloartenol, 24-methylene cycloartenol, obtusifoliol,

20 stigmasta-7-enol and campesterol) in their storage organs relative to an otherwise identical transgenic plant transformed only with a truncated HMG-CoA reductase gene. Nucleic acid sequences encoding enzymes that affect the biosynthesis and accumulation of steroid compounds in plants

25 (HMG-CoA reductase and a steroid pathway enzyme), and methods for using these sequences to produce such transgenic plants, are also provided. These methods comprise, for example, introducing into cells nucleic acid sequences encoding enzymes that affect the levels of accumulated

30 steroid pathway end products.

The present invention contemplates a recombinant construct or a recombinant vector that contains 2 DNA sequences. The first encodes a polypeptide exhibiting 3-hydroxy-3-methylglutaryl-Coenzyme A (HMG-CoA) reductase

activity. The second DNA sequence encodes a polypeptide exhibiting the activity of another steroid pathway enzyme. Each polypeptide-encoding DNA sequence is operably linked in the 5' to 3' direction to a promoter and a transcription termination signal sequence independent of the other sequence. The promoter is located upstream and the termination sequence downstream of each polypeptide-encoding DNA sequence. The second DNA sequence encoding a steroid pathway enzyme can code for a squalene epoxidase enzyme, a sterol methyl transferase I enzyme, a sterol C4-demethylase enzyme, a obtusifolioside C14 α -demethylase enzyme, a sterol C5-desaturase enzyme, or a sterol methyl transferase II enzyme. It is contemplated that HMG-CoA reductase and the steroid pathway enzyme activity comes from a mutant or truncated form of those enzymes, such as a truncated HMG-CoA reductase lacking the transmembrane region while retaining a functional catalytic domain. Examples of such preferred HMG CoA reductases include the truncated rubber and *Arabidopsis* HMG CoA reductases disclosed herein.

Preferably, the regulatory function of a promoter is substantially unaffected by cellular levels of squalene such as the CaMV 35S promoter. In one aspect, a promoter is seed-specific. In another aspect, a promoter is derived from a species in a different order from a host cell. In another aspect, the HMG-CoA reductase or steroid pathway enzymes is from a species in a different order from the order that of the host cell. The invention contemplates a construct or recombinant vector having more than one DNA sequence encoding a steroid pathway enzyme that do not have to be under the control of the same promoter. Preferably, a recombinant vector is a plant expression vector.

In another aspect of the invention, a transformed host cell comprises a recombinant construct or vector as described above. Preferably, a host cell is plant cell,

preferably that plant cell is from canola, soybean, corn, maize, tobacco, cotton, rape, tomato or alfalfa. The invention contemplates a host cell in a cell culture, plants derived from transformed host cells, and storage organs
5 (seeds, fruits and vegetable parts) from transgenic plants.

In addition to contemplating transgenic plants and seeds, the invention contemplates transgenic plant seeds capable of germinating into a transgenic plant and mutants, recombinants, genetically engineered derivatives thereof and
10 hybrids derived therefrom. The plant over-accumulates steroid pathway products relative to a native, non-transgenic plant of the same strain, wherein said mutants, recombinants, genetically engineered derivatives thereof and hybrids derived therefrom maintain the ability to
15 overaccumulate steroid pathway products.

The invention contemplates a process of increasing the formation of steroid pathway products in a transformed host cell as compared to an otherwise identical non-transformed host cell. Contemplated processes use the described
20 recombinant constructs and vectors to transform host cells, then growing the host cells or regenerating transgenic plants therefrom.

In one aspect of the invention, the genome of a contemplated plant, its progeny, seeds or cell culture,
25 comprises introduced DNA encoding an HMG-CoA reductase activity and introduced DNA encoding a steroid pathway enzyme that is a squalene epoxidase enzyme, a sterol methyl transferase I enzyme, a sterol C4-demethylase enzyme, a obtusifoliol C14 α -demethylase enzyme, a sterol C5-desaturase
30 enzyme, or a sterol methyl transferase II enzyme. The storage organs of such a plant contain an elevated level of total accumulated sterol, compared to storage organs of an otherwise identical plant, the genome of which does not comprise said introduced DNA. Further, the storage organs

of the plant contain a reduced level of squalene, cycloartenol, 24-methylene cycloartenol, obtusifoliol, stigmasta-7-enol, or campesterol compared to the seeds of an otherwise identical plant or a plant comprising an introduced DNA encoding an HMG-CoA reductase enzyme.

The invention contemplates a method of producing a plant that accumulates an elevated level of sterol pathway products compared to a corresponding plant comprising no introduced DNA encoding a peptide, polypeptide, or protein that affects the biosynthesis and accumulation of a sterol pathway product, comprising sexually crossing plants to arrive at a plant comprising nucleic acid encoding an HMG CoA reductase and a steroid pathway enzyme, including crosses with a nurse cultivar. The plants, including apomictic plants, uniform populations of the plants and their seeds and parts other than seeds are contemplated.

Another aspect of the invention is oils containing at least one sterol pathway product, extracted from the seeds of a contemplated plant. Preferably sitosterol, at least one sitosterol ester, or mixtures thereof, comprise at least about 57% by weight of the total sterol compounds of a contemplated oil. Preferably sitosterol, that at least one sitosterol ester, or mixtures thereof, comprise at least about 0.08% of the dry weight of a contemplated seed. Preferably, the oil has a reduced amount of squalene, cycloartenol, 24-methylene cycloartenol, obtusifoliol, stigmasta-7-enol, campesterol, or combinations thereof, compared to oil from a corresponding transgenic plant that does not contain introduced DNA encoding a squalene epoxidase enzyme, a sterol methyl transferase I enzyme, a sterol C4-demethylase enzyme, a obtusifoliol C14 α -demethylase enzyme, a sterol C5-desaturase enzyme, a sterol methyl transferase II enzyme, or mixture thereof; wherein

the reduction is in the range of from about 10% to about 100%.

Sitosterol ester compositions derived from transgenic plants of the present invention, their progeny or their
5 seeds are also contemplated, preferably wherein an esterifying fatty acid has 2 to 22 carbon atoms in the main chain.

A further aspect of the invention is cholesterol-lowering compositions comprising contemplated oils and
10 sitosterol ester compositions. Another further aspect of the invention is foods, food ingredients, or food compositions comprising contemplated oils.

Still further, the invention contemplates pharmaceutical compositions comprising a cholesterol-lowering effective amount of a contemplated oil, and a
15 pharmaceutically acceptable carrier, excipient, or diluent.

A method of lowering the plasma concentration of low density lipoprotein cholesterol is contemplated, comprising orally administering to a human or animal subject an
20 effective amount of an above composition. Also contemplated is a method of treating or preventing an elevated plasma concentration of low-density lipoprotein cholesterol, comprising orally administering to a human or animal subject an effective amount of a contemplated composition.

25 A related aspect of the invention is a method of making a food additive composition, comprising obtaining oil containing a sterol pathway product compound from seed of a contemplated transgenic plant and mixing the oil with an edible solubilizing agent, an effective amount of a
30 dispersant, and optionally, an effective amount of an antioxidant.

Novel forms of two sterol pathway enzymes and the nucleic acids that encode them are disclosed: an *Arabidopsis* enzyme having nucleic acid similarity to a squalene

epoxidase, and an *Arabidopsis* enzyme having nucleic acid similarity to an obtusifoliol C14 α -demethylase enzyme. Thus, the invention contemplates an isolated DNA molecule having a nucleotide sequence of disclosure SEQ ID NO: 4, 6, 8, 10, 14, 15, 17 or the complements thereof. Also contemplated is a nucleotide sequence that hybridizes to the nucleotide sequence of SEQ ID NO: 4, 6, 8, 10, 14, 15, 17 or their complements under a wash stringency equivalent to 0.5X SSC to 2X SSC, 0.1% SDS, at 55-65°C, and that encode a polypeptide having squalene epoxidase or obtusifoliol C14 α -demethylase enzymatic activity. Preferably, that enzymatic activity is substantially similar to that of a disclosed squalene epoxidase or obtusifoliol C14 α -demethylase, respectively. By substantially similar is meant having enzymatic activity differing from that of the disclosed enzymes by about 30% or less, preferably by about 20% or less, and more preferably by about 10% or less when assayed by standard enzymatic assays. Also contemplated is a nucleotide sequence encoding the same genetic information as said nucleotide sequence of SEQ ID NO: 4, 6, 8, 10, 14, 15, 17 or their complements or that hybridize as described above, but which is degenerate in accordance with the degeneracy of the genetic code. Recombinant constructs, vectors and transformed host cells comprising the novel isolated and purified nucleic acid sequences are also contemplated. In one embodiment, the vector is a plant vector and the host cell is a plant cell. Methods of producing the disclosed squalene epoxidase or obtusifoliol C14 α -demethylase enzymes are also contemplated comprising culturing a transformed host cell for a time and under conditions conducive to the production of the squalene epoxidase or obtusifoliol C14 α -demethylase enzyme, and

recovering the produced squalene epoxidase or obtusifolioside C14 α -demethylase enzyme.

Yet another aspect provides any of the above described transformed host cells, further comprising a recombinant construct or expression vector encoding a tocopherol
5 synthesis pathway enzyme, and in particular, S-adenosylmethionine-dependent α -tocopherol methyltransferase. Also included are plants, seeds and storage organs comprising the transformed host cells.

10 Another aspect provides, a process of increasing the formation of steroid pathway products and tocopherols in a transformed host cell as compared to an otherwise identical non-transformed host cell comprising (1) transforming a host cell with a recombinant vector comprising (a) as operably
15 linked components in the 5' to 3' direction, a promoter, a DNA sequence encoding a first polypeptide having 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity, and a transcription termination signal sequence; and (b) as operably linked components in the 5' to 3' direction, a
20 promoter, a DNA sequence encoding at least one polypeptide having steroid pathway enzyme activity selected from the group consisting of squalene epoxidase enzyme activity, sterol methyl transferase I enzyme activity, sterol C4-demethylase enzyme activity, obtusifolioside C14 α -demethylase
25 enzyme activity, sterol C5-desaturase enzyme activity, and sterol methyl transferase II enzyme activity, and a transcription termination signal sequence; (2) transforming the host cell of (1) with a recombinant vector comprising as operably linked components, a promoter, a DNA sequence
30 encoding a tocopherol synthesis pathway enzyme, and a transcription termination sequence; and (3) regenerating said transformed plant cell into said transgenic plant.

BRIEF DESCRIPTION OF THE DRAWINGS

These and other features, aspects, and advantages of the present invention will become better understood with regard to the following description, appended claims and
5 accompanying figures where:

Fig. 1 is an abbreviated version of a plant steroid compound biosynthetic pathway that shows the enzymes affecting steroid compound biosynthesis and accumulation.

10 These include: HMG-CoA reductase, squalene epoxidase, sterol methyl transferase I, sterol C4-demethylase, obtusifoliol C14 α -demethylase, sterol C5 desaturase and sterol methyl transferase II.

Fig. 2 depicts the forms of *Arabidopsis* and rubber. HMGR1 tested in *Arabidopsis* and yeast to compare expression,
15 activity and sterol production.

Fig. 3 is a map showing the structure of construct pMON29920. pMON29920 is a binary transformation vector with P-7S/E9 3' cassette and the KAN gene flanked by the two
20 borders where P-7S is the promoter of alpha' beta conglycinin protein from soybean, E9 3' is the 3' end of pea rbc E9 gene and KAN is the coding sequence for NPTII that confers resistance to kanamycin. The NPTII gene is driven by the 35S promoter from cauliflower mosaic virus. Spc.Str
25 is the coding region for Tn7 adenyltransferase conferring resistance to spectinomycin and streptomycin; ori-V: the vegetative origin of replication; rop: coding region for repressor of primer; ori-322: minimum known sequence required for a functional origin of replication; NOS 3': the
30 3' termination end of nopaline synthase coding region.

Fig. 4 is a map showing the structure of construct pMON43800. pMON43800 is a recombinant binary vector for Agrobacterium-mediated transformation, carrying the rubber HMGR1 gene cassette. The HMGR1 gene is driven by the 7S

alpha' beta conglycinin promoter from soybean. P-7S: 7S promoter, rubber HMGR1 gene: coding sequence for 3-hydroxy-3-methylglutaryl reductase from *Hevea brasiliensis*; E9 3': 3' end of pea rbcS E9 gene; P-35S: 35S promoter from
 5 cauliflower mosaic virus; KAN: coding region for NPTII gene conferring resistance for kanamycin; NOS 3': 3' termination end of nopaline synthase coding region: Left Border: Octapine left border from Octapine Ti plasmid pTiA6; ori-V: the vegetative origin of replication; rop: coding region for
 10 repressor of primer; Spc/Str: coding region for Tn7 adenylyltransferase conferring resistance to spectinomycin and streptomycin.

Fig. 5 is a map showing the structure of construct pMON23616. pMON23616 is a plant expression vector
 15 containing P-NOS/ORF-7/KAN/NOS-3' cassette. P-NOS: NOS promoter from *Agrobacterium tumefaciens* pTiT37; ORF-7: a short open reading frame that attenuates expression of KAN in plants; KAN: coding sequence of NPTII gene that confers resistance to kanamycin and neomycin; ble: confers
 20 resistance to bleomycin; NOS 3': 3' termination end of nopaline synthase coding region; Left Border: Octapine left border from Octapine Ti plasmid pTiA6; ori-V: the vegetative origin of replication; rop: coding region for repressor of primer; Spc/Str: coding region for Tn7 adenylyltransferase
 25 conferring resistance to spectinomycin and streptomycin.

Fig. 6 is a map showing the structure of construct pMON43818. pMON43818 is a recombinant binary vector carrying the gene encoding rubber hydroxymethyl glutaryl CoA reductase1 (HMGR1) in sense orientation driven by the
 30 soybean alpha' beta conglycinin promoter. P-NOS: nopaline synthase gene promoter; kan: coding region for neomycin phospho transferase protein to confer resistance to kanamycin; NOS 3': 3' termination end of nopaline synthase coding region; Soy Alpha' Beta Conglycinin: 7S alpha' beta

conglycinin gene promoter from soybean; Rubber HMGR1 gene:
coding sequence for HMGR1 gene from *Hevea brasiliensis*; E9
3': 3' end of pea rbcS E9 gene; Left border: octopine left
border, sequence essential for transfer of T-DNA into
5 *Agrobacterium*; ori-V: plasmid origin of replication in
Agrobacterium; rop: coding sequence for repressor of primer;
Ori-322: origin of replication in *E.coli*; Spc/Str: coding
region for Tn7 adenyltransferase (AAD(3")) conferring
resistance to spectinomycin and streptomycin; Right Border:
10 right border sequence of T-DNA essential for integration
into *Agrobacterium*.

Figure 7 is a map showing the structure of construct
pMON43052. pMON43052 is a recombinant shuttle vector,
carrying the cDNA fragment encoding the catalytic domain of
15 *Arabidopsis* HMGR1 in sense orientation driven by the soybean
alpha' beta conglycinin promoter. P-NOS: nopaline synthase
gene promoter; kan: coding region for neomycin
phosphotransferase protein to confer resistance to
kanamycin; NOS 3': 3' termination end of nopaline synthase
20 coding region; Soy Alpha' Beta Conglycinin: 7S alpha' beta
conglycinin gene promoter from soybean; *Arabidopsis* HMGR
catalytic domain: coding sequence for the catalytic domain
of *Arabidopsis* HMGR1 protein; E9 3': 3' end of pea rbcS E9
gene; Left border: octopine left border, sequence essential
25 for transfer of T-DNA into *Agrobacterium*; ori-V: plasmid
origin of replication in *Agrobacterium*; rop: coding sequence
for repressor of primer; Ori-322: origin of replication in
E.coli; Spc/Str: coding region for Tn7 adenyltransferase
(AAD(3")) conferring resistance to spectinomycin and
30 streptomycin; Right Border: right border sequence of T-DNA
essential for integration into *Agrobacterium*.

Figure 8 is a map showing the structure of construct
pMON51850. pMON51850 is a binary vector for *Agrobacterium*
mediated transformation of soybean. P-NOS: nopaline

synthase gene promoter; kan: coding region for neomycin phosphotransferase protein to confer resistance to kanamycin; NOS 3': 3' termination end of nopaline synthase coding region; Left border: octopine left border sequence
 5 essential for transfer of T-DNA into *Agrobacterium*; ori-V: plasmid origin of replication in *Agrobacterium*; rop: coding sequence for repressor of primer; ori-322: origin of replication in *E.coli*; Spc/Str: coding region for Tn7 adenylyltransferase (AAD(3")) conferring resistance to
 10 spectinomycin and streptomycin; Right Border: right border sequence of T-DNA essential for integration into *Agrobacterium*.

Figure 9 is a map showing the structure of construct pMON43057. pMON43057 is a recombinant binary vector for
 15 *Agrobacterium* mediated transformation of soybean, carrying the gene cassette for expressing catalytic domain of HMGR1 from *Arabidopsis thaliana*. The catalytic domain of the HMGR1 cDNA is driven by soybean 7S alpha' beta conglycinin promoter. P-NOS: nopaline synthase gene promoter; kan:
 20 coding region for neomycin phosphotransferase protein to confer resistance to kanamycin; NOS 3': 3' termination end of nopaline synthase coding region; Left border: octopine left border sequence essential for transfer of T-DNA into *Agrobacterium*; ori-V: plasmid origin of replication in
 25 *Agrobacterium*; rop: coding sequence for repressor of primer; ori-322: origin of replication in *E.coli*; Spc/Str: coding region for Tn7 adenylyltransferase (AAD(3")) conferring resistance to spectinomycin and streptomycin; Right Border: right border sequence essential for transfer of T-DNA into
 30 *Agrobacterium*; Soy Alpha' Beta Conglycinin: soybean 7S alpha' beta conglycinin gene promoter; *Arabidopsis* HMGR catalytic domain: coding sequence for *Arabidopsis* HMGR1 catalytic domain; E9 3': 3' end of pea rbcS E9 gene.

Figure 10 is a map showing the structure of construct pMON43058. pMON43058 is a recombinant binary vector for *Agrobacterium*-mediated soybean transformation, carrying gene expression cassettes for catalytic domain of HMGR1 from *Arabidopsis thaliana* and SMTII from *Arabidopsis thaliana*. P-NOS: nopaline synthase gene promoter; kan: coding region for neomycin phosphotransferase protein to confer resistance to kanamycin; NOS 3': 3' termination end of nopaline synthase coding region; Left border: octopine left border sequence essential for transfer of T-DNA into *Agrobacterium*; ori-V: plasmid origin of replication in *Agrobacterium*; rop: coding sequence for repressor of primer; ori-322: origin of replication in *E.coli*; Spc/Str: coding region for Tn7 adenyltransferase (AAD(3")) conferring resistance to spectinomycin and streptomycin; Right Border: right border sequence essential for transfer of T-DNA into *Agrobacterium*; Soy Alpha' Beta Conglycinin: 7S alpha' beta conglycinin gene promoter from soybean; *Arabidopsis* HMGR catalytic domain: sequence encoding the catalytic domain of *Arabidopsis* HMGR1; E9 3': 3' end of pea rbcS E9 gene; Soy Alpha' Beta Conglycinin: soybean 7S alpha'beta conglycinin gene promoter; *Arabidopsis* SMT2: cDNA encoding sterol methyl transferase II enzyme from *Arabidopsis thaliana* (accession no: X89867); NOS 3': 3' termination end of nopaline synthase coding region.

Fig. 11 is profile (histogram) of the sterol composition of R1 transgenic soybean seeds when *Arabidopsis* truncated HMGR (catalytic domain without linker) was overexpressed using seed-specific 7S promoter (data from pMON43057:p7S::At HMGR truncated).

Fig. 12 is a profile (histogram) of the sterol composition of R1 transgenic soybean seeds when *Arabidopsis* truncated HMGR (catalytic domain without linker) and *Arabidopsis* SMTII were overexpressed (data from

pMON43058:p7S::At HMGR truncated and p7S::At SMTII). The expression of the genes is controlled by the seed-specific 7S promoter.

Figure 13 is a map showing the structure of construct pMON53733. pMON53733 is a recombinant binary vector carrying the cDNA encoding full-length form of *Arabidopsis* hydroxymethyl glutaryl CoA reductase1 (HMGR1) in sense orientation driven by the enhanced cauliflower mosaic virus 35S promoter. P-35S: 35S promoter from cauliflower mosaic virus; kan: confers resistance to neomycin and kanamycin; NOS 3': 3' termination end of nopaline synthase coding region; Left border: octopine left border, sequence essential for transfer of T-DNA into *Agrobacterium*; ori-V: plasmid origin of replication in *Agrobacterium*; rop: coding sequence for repressor of primer; ori-322: origin of replication in *E.coli*; Spc/Str: coding region for Tn7 adenyltransferase (AAD(3")) conferring resistance to spectinomycin and streptomycin; Right Border: right border sequence of T-DNA essential for integration into *Agrobacterium*; P-e35S: enhanced cauliflower mosaic virus promoter; *Arabidopsis* HMGR1: cDNA sequence encoding full-length form of *Arabidopsis* HMGR1; E9 3': 3' end of pea rbcS E9 gene.

Figure 14 is a map showing the structure of construct pMON53734. pMON53734 is a recombinant binary vector carrying the cDNA encoding catalytic domain with linker region of *Arabidopsis* hydroxymethyl glutaryl CoA reductase1 (HMGR1) in sense orientation driven by the enhanced cauliflower mosaic virus 35S promoter. P-35S: 35S promoter from cauliflower mosaic virus; kan: confers resistance to neomycin and kanamycin; NOS 3': 3' termination end of nopaline synthase coding region; Left border: octopine left border, sequence essential for transfer of T-DNA into *Agrobacterium*; ori-V: plasmid origin of replication in

Agrobacterium; rop: coding sequence for repressor of primer; ori-322: origin of replication in *E.coli*; Spc/Str: coding region for Tn7 adenyllyltransferase (AAD(3")) conferring resistance to spectinomycin and streptomycin; Right Border: right border sequence of T-DNA essential for integration into *Agrobacterium*; P-e35S: enhanced cauliflower mosaic virus promoter; *Arabidopsis* tHMGR1: cDNA sequence encoding catalytic domain with linker region of *Arabidopsis* HMGR1; E9 3': 3' end of pea rbcS E9 gene.

Figure 15 is a map showing the structure of construct pMON53735. pMON53735 is a recombinant binary vector carrying the cDNA encoding catalytic domain without the linker region of *Arabidopsis* hydroxymethyl glutaryl CoA reductase1 (HMGR1) in sense orientation driven by the enhanced cauliflower mosaic virus 35S promoter. P-35S: 35S promoter from cauliflower mosaic virus; kan: confers resistance to neomycin and kanamycin; NOS 3': 3' termination end of nopaline synthase coding region; Left border: octopine left border, sequence essential for transfer of T-DNA into *Agrobacterium*; ori-V: plasmid origin of replication in *Agrobacterium*; rop: coding sequence for repressor of primer; ori-322: origin of replication in *E.coli*; Spc/Str: coding region for Tn7 adenyllyltransferase (AAD(3")) conferring resistance to spectinomycin and streptomycin; Right Border: right border sequence of T-DNA essential for integration into *Agrobacterium*; P-e35S: enhanced cauliflower mosaic virus promoter; *Arabidopsis* cHMGR1: cDNA sequence encoding catalytic domain without the linker region of *Arabidopsis* HMGR1; E9 3': 3' end of pea rbcS E9 gene.

Figure 16 is a map showing the structure of construct pMON53736. pMON53736 is a recombinant binary vector carrying the cDNA encoding full-length form of rubber (*Hevea brasiliensis*) hydroxymethyl glutaryl CoA reductase1 (HMGR1) in sense orientation driven by the enhanced cauliflower

mosaic virus 35S promoter. P-35S: 35S promoter from cauliflower mosaic virus; kan: confers resistance to neomycin and kanamycin; NOS 3': 3' termination end of nopaline synthase coding region; Left border: octopine left border, sequence essential for transfer of T-DNA into *Agrobacterium*; ori-V: plasmid origin of replication in *Agrobacterium*; rop: coding sequence for repressor of primer; ori-322: origin of replication in *E.coli*; Spc/Str: coding region for Tn7 adenyltransferase (AAD(3")) conferring resistance to spectinomycin and streptomycin; Right Border: right border sequence of T-DNA essential for integration into *Agrobacterium*; P-e35S: enhanced cauliflower mosaic virus promoter; Hevea HMGR1: cDNA sequence encoding full-length form of rubber HMGR1; E9 3': 3' end of pea rbcS E9 gene.

Figure 17 is a map showing the structures of construct pMON53737. pMON53737 is a recombinant binary vector carrying the cDNA encoding catalytic domain with linker region of rubber (*Hevea brasiliensis*) hydroxymethyl glutaryl CoA reductase1 (HMGR1) in sense orientation driven by the enhanced cauliflower mosaic virus 35S promoter. P-35S: 35S promoter from cauliflower mosaic virus; kan: confers resistance to neomycin and kanamycin; NOS 3': 3' termination end of nopaline synthase coding region; Left border: octopine left border, sequence essential for transfer of T-DNA into *Agrobacterium*; ori-V: plasmid origin of replication in *Agrobacterium*; rop: coding sequence for repressor of primer; ori-322: origin of replication in *E.coli*; Spc/Str: coding region for Tn7 adenyltransferase (AAD(3")) conferring resistance to spectinomycin and streptomycin; Right Border: right border sequence of T-DNA essential for integration into *Agrobacterium*; P-e35S: enhanced cauliflower mosaic virus promoter; rubber tHMGR1: cDNA sequence encoding

catalytic domain with linker region of rubber HMGR1; E9 3': 3' end of pea rbcS E9 gene.

Figure 18 is a map showing the structure of construct pMON53738. pMON53738 is a recombinant binary vector

5 carrying the cDNA encoding mutant form of rubber (*Hevea brasiliensis*) hydroxymethyl glutaryl CoA reductase1 (HMGR1) in sense orientation driven by the enhanced cauliflower mosaic virus 35S promoter. In the mutant rubber HMGR1 the putative phosphorylation site, the serine amino acid residue

10 at position 566 is changed to alanine amino acid residue (SEQ ID 23). P-35S: 35S promoter from cauliflower mosaic virus; kan: confers resistance to neomycin and kanamycin; NOS 3': 3' termination end of nopaline synthase coding region; Left border: octopine left border, sequence

15 essential for transfer of T-DNA into *Agrobacterium*; ori-V: plasmid origin of replication in *Agrobacterium*; rop: coding sequence for repressor of primer; ori-322: origin of replication in *E.coli*; Spc/Str: coding region for Tn7 adenyltransferase (AAD(3")) conferring resistance to

20 spectinomycin and streptomycin; Right Border: right border sequence of T-DNA essential for integration into *Agrobacterium*; P-e35S: enhanced cauliflower mosaic virus promoter; rubber tHMGR1 Ala 566: cDNA sequence encoding catalytic domain with linker region of rubber HMGR1 in which

25 serine amino acid residue at position 566 is changed to alanine amino acid residue using site directed mutagenesis; E9 3': 3' end of pea rbcS E9 gene.

Figure 19 is a map showing the structure of construct pMON53739. pMON53739 is a recombinant binary vector

30 carrying the cDNA encoding mutant form of rubber (*Hevea brasiliensis*) hydroxymethyl glutaryl CoA reductase1 (HMGR1) in sense orientation driven by the enhanced cauliflower mosaic virus 35S promoter. In the mutant rubber HMGR1 the putative phosphorylation site, the serine amino acid residue

at position 567 is changed to alanine amino acid residue (SEQ ID 24). P-35S: 35S promoter from cauliflower mosaic virus; kan: confers resistance to neomycin and kanamycin; NOS 3': 3' termination end of nopaline synthase coding region; Left border: octopine left border, sequence essential for transfer of T-DNA into *Agrobacterium*; ori-V: plasmid origin of replication in *Agrobacterium*; rop: coding sequence for repressor of primer; ori-322: origin of replication in *E.coli*; Spc/Str: coding region for Tn7 adenylyltransferase (AAD(3")) conferring resistance to spectinomycin and streptomycin; Right Border: right border sequence of T-DNA essential for integration into *Agrobacterium*; P-e35S: enhanced cauliflower mosaic virus promoter; rubber tHMGR1 Ala 567: cDNA sequence encoding catalytic domain with linker region of rubber HMGR1 in which serine amino acid residue at position 567 is changed to alanine amino acid residue using site directed mutagenesis; E9 3': 3' end of pea rbcS E9 gene.

Figure 20 is a map showing the structure of construct pMON53740. pMON53740 is a recombinant binary vector carrying the cDNA encoding catalytic domain without linker region of rubber (*Hevea brasiliensis*) hydroxymethyl glutaryl CoA reductase1 (HMGR1) in sense orientation driven by the enhanced cauliflower mosaic virus 35S promoter. P-35S: 35S promoter from cauliflower mosaic virus; kan: confers resistance to neomycin and kanamycin; NOS 3': 3' termination end of nopaline synthase coding region; Left border: octopine left border, sequence essential for transfer of T-DNA into *Agrobacterium*; ori-V: plasmid origin of replication in *Agrobacterium*; rop: coding sequence for repressor of primer; ori-322: origin of replication in *E.coli*; Spc/Str: coding region for Tn7 adenylyltransferase (AAD(3")) conferring resistance to spectinomycin and streptomycin; Right Border: right border sequence of T-DNA essential for

integration into *Agrobacterium*; P-e35S: enhanced cauliflower mosaic virus promoter; rubber cHMGR1: cDNA sequence encoding catalytic domain without linker region of rubber HMGR1; E9 3': 3' end of pea rbcS E9 gene.

5 Fig. 21 is a graph comparing the cycloartenol content in micrograms of steroid compound per gram of seeds analyzed in transgenic *Arabidopsis* plants transformed with pMON53733 through pMON53740 compared to control plants.

Fig. 22 is a graph comparing the 24-methylene
10 cycloartenol content in micrograms of steroid compound per gram of seeds analyzed in transgenic *Arabidopsis* plants transformed with pMON53733 through pMON53740 compared to control plants.

Fig. 23 is a graph comparing the obtusifoliol content
15 in micrograms of steroid compound per gram of seeds analyzed in transgenic *Arabidopsis* plants transformed with pMON53733 through pMON53740 compared to control plants.

Fig. 24 is a graph comparing the campesterol content in micrograms of steroid compound per gram of seeds analyzed in
20 transgenic *Arabidopsis* plants transformed with pMON53733 through pMON53740 compared to control plants.

Fig. 25 is a graph comparing the sitosterol content in micrograms of steroid compound per gram of seeds analyzed in transgenic *Arabidopsis* plants transformed with pMON53733
25 through pMON53740 compared to control plants.

Fig. 26 is a graph comparing the sitostanol content in micrograms of steroid compound per gram of seeds analyzed in transgenic *Arabidopsis* plants transformed with pMON53733 through pMON53740 compared to control plants.

30 Fig. 27 is a sterol profile (histogram) of transgenic *Arabidopsis* harboring different forms of rubber HMGR.

Fig. 28 is a graph of the squalene, zymosterol and erogosterol content in micrograms of sterol per milligram of cell dry weight from HMGR constructs in yeast HMGR1 knockout

mutants for constructs having full length and truncated HMG CoA reductase (HMGR) sequences. The truncated sequences contain substantial portions of the catalytic region but lack the linker region and the transmembrane region of HMGR. These sequences are derived from *Arabidopsis* and rubber plants.

Fig. 29 is a map showing the structure of construct pMON43842. pMON43842 is a yeast expression vector carrying cDNA encoding *Arabidopsis* putative obtusifoliol C14 α -demethylase (AC002329) in sense orientation driven by the p423Gall1 promoter. Sc.His3: HIS3 region from *Saccharomyces cerevisiae* encoding imidazoleglycerol-phosphate dehydratase for histidine synthesis; Ori-f1: bacteriophage f1 origin of replication; LAC: contains partial lacI coding sequence, promoter Plac, promoter Pt7, promoter Pt3, KS polylinker, and partial lacZ coding sequence; lacZ: partial coding sequence for beta-d-galactosidase or lacZ protein; T-Sc.Cycl: a terminator from Cycl- iso-1-cytochrome c from *Saccharomyces cerevisiae* to terminate transcription; obtus. C14 α .demethylase (AC002329): cDNA encoding *Arabidopsis* putative obtusifoliol C14 α -demethylase; P-Sc.Gall1: a promoter from Gall1- galactokinase of *Saccharomyces cerevisiae* to direct expression with galactose induction; LacZ-alpha: partial coding sequence for beta-d-galactosidase or lacZ protein; Ori-pUC: minimum sequence required for a functional origin of replication, sequence downstream of this region is known to affect copy number when expressed in bacteria; AMP: contains the P3 promoter and the beta-lactamase coding sequence, conferring resistance to ampicillin, penicillin, and carbenicillin; Sc.2micron: 2 micron origin of replication.

Fig. 30 is a map showing the structure of construct pMON43843. pMON43843 is a yeast expression vector carrying

cDNA encoding *Arabidopsis* putative squalene epoxidase 1 (ATA506263) in sense orientation driven by the p423Gall promoter. Sc.His3: HIS3 region from *Saccharomyces cerevisiae* encoding imidazoleglycerol-phosphate dehydratase for histidine synthesis; Ori-f1: bacteriophage f1 origin of replication; LAC: contains partial lacI coding sequence, promoter Plac, promoter Pt7, promoter Pt3, KS polylinker, and partial lacZ coding sequence; lacZ: partial coding sequence for beta-d-galactosidase or lacZ protein; T-Sc.Cycl1: a terminator from Cycl1- iso-1-cytochrome c from *Saccharomyces cerevisiae* to terminates transcription; Squalene epoxidase 1 (ATA506263): cDNA encoding *Arabidopsis* putative squalene epoxidase 1 (ATA506263); P-Sc.Gall: a promoter from Gall- galactokinase of *Saccharomyces cerevisiae* to direct expression with galactose induction; LacZ-alpha: partial coding sequence for beta-d-galactosidase or lacZ protein; Ori-pUC: minimum sequence required for a functional origin of replication, sequence downstream of this region is known to affect copy number when expressed in bacteria; AMP: contains the P3 promoter and the beta-lactamase coding sequence, conferring resistance to ampicillin, penicillin, and carbenicillin; Sc.2micron: 2 micron origin of replication.

Fig. 31 is a map showing the structure of construct pMON43844. pMON43844 is a yeast expression vector carrying cDNA encoding *Arabidopsis* putative squalene epoxidase 1 (ATA304243) in sense orientation driven by the p423Gall promoter. Sc.His3: HIS3 region from *Saccharomyces cerevisiae* encoding imidazoleglycerol-phosphate dehydratase for histidine synthesis; Ori-f1: bacteriophage f1 origin of replication; LAC: contains partial lacI coding sequence, promoter Plac, promoter Pt7, promoter Pt3, KS polylinker, and partial lacZ coding sequence; lacZ: partial coding sequence for beta-d-galactosidase or lacZ protein; T-

Sc.Cycl1: a terminator from Cycl1- iso-1-cytochrome c from *Saccharomyces cerevisiae* to terminate transcription; Arab. squalene epoxidase 1 (ATA304243): cDNA encoding *Arabidopsis* putative squalene epoxidase 1 (ATA304243); P-Sc.Gal1: a
 5 promoter from Gal1- galactokinase of *Saccharomyces cerevisiae* to direct expression with galactose induction; LacZ-alpha: partial coding sequence for beta-d-galactosidase or lacZ protein; Ori-pUC: minimum sequence required for a functional origin of replication, sequence downstream of
 10 this region is known to affect copy number when expressed in bacteria; AMP: contains the P3 promoter and the beta-lactamase coding sequence, conferring resistance to ampicillin, penicillin, and carbenicillin; Sc.2micron: 2 micron origin of replication.

15 Fig. 32 is a comparison of known HMG CoA reductase amino acid sequences. ClustalW alignment of forty-three non-redundant HMG-CoA reductase sequences to represent archaeobacterial, eubacterial, fungal, plant and animal groups. The putative functional domains in the alignment
 20 marked as described below are based on the three dimensional structure of *Pseudomonas mevalonii* HMGR (Lawrence et al., 1995, Science 268:1758): boxed-HMGCoA binding domain, light shade-NAD(H) binding domain, underlined consensus- domains involved in catalysis, *
 25 underneath consensus and boldface-key histidine residue involved in catalysis. The putative phosphorylation site residues are marked with ‡ and boldface, and are located at the C-terminal region of the protein, adjacent to a highly conserved arginine, marked with † and boldface. Also
 30 indicated are the conserved Glu (E), Lys (K), and Asp (D) residues, marked by E, K, and D, respectively. These residues are thought to be critical in catalysis, based on the crystal structure (Tabernero et al., 1999; PNAS 96(13):7167-71).

Appendices A through C show SEQ ID Nos: 1 through 3, respectively. Appendices D through G show SEQ ID Nos 20 thorough 23, respectively.

5 DETAILED DESCRIPTION

The following detailed description is provided to aid those skilled in the art in practicing the present invention. Even so, this detailed description should not be construed to unduly limit the present invention as
10 modifications and variations in the embodiments discussed herein can be made by those of ordinary skill in the art without departing from the spirit or scope of the present inventive discovery.

All publications, patents, patent applications,
15 databases and other references cited in this application are herein incorporated by reference in their entirety as if each individual publication, patent, patent application, database or other reference were specifically and individually indicated to be incorporated by reference.

20 We have expressed the full-length forms of the rubber and *Arabidopsis* HMGRs driven by seed-specific promoters in transgenic canola and soybean. We have demonstrated sterol over-production up to 2-4 fold higher in seeds from these transgenic plants. We also demonstrated a higher
25 accumulation of pathway intermediates in soybean than canola. These results were disclosed in PCT publication WO 00/61771. However, we have expressed a truncated form of the *Arabidopsis hmg1* without the linker and membrane spanning domains in *Arabidopsis* and soybean. The results in
30 *Arabidopsis* were similar to that demonstrated by Gonzalez et al. (1997) and we compared the sterol profiles of our transgenic plants with those produced by Gonzalez et al., using our methods to show they are comparable. We found the same types of pathway intermediates accumulating. However,

in soybean seeds we have demonstrated the accumulation of squalene to a very high level (~3mg/g seed which is around 100-fold higher than in nontransgenic controls). This is an unexpected result not disclosed or suggested in the prior art. Squalene is a precursor for sterols and in soybean it appears that there is a "bottleneck" in the further conversion of this precursor to sterols. Thus, it appears that there could be additional ways of over-producing sterols in soybean to levels greater than 10-fold which would include combining a truncated form of HMGR with other genes coding for enzymes down-stream of squalene.

This opens the potential to combine other genes such as squalene epoxidase for further enhancing the levels of desirable sterols. Such a combination has not been disclosed or suggested in the prior art. Squalene epoxidase catalyzes the addition of oxygen to squalene which is a 30-carbon linear isoprenoid chain thus allowing for cyclization to form cycloartenol. Additional enzymes downstream that can be also be manipulated are sterol methyltransferase 1, C-4 demethylase, C-14 demethylase, sterol methyltransferase 2, and C-5 desaturase that would all deplete other pathway intermediates shown to accumulate in soybeans. By using such strategies it is possible to convert all of the squalene and other intermediates to end sterols such as sitosterol, stigmasterol and campesterol. Thus, sterol level in soybean oils can be elevated from 0.3% up to 3.5%. Expression of the full-length rubber HMGR in soybeans results in a sterol level increase up to 2.7%.

Enhancement of 3-hydroxy-3-methylglutaryl-CoA reductase (HMG Co-A reductase) activity in certain cells results in increased sterol biosynthesis. See, e.g. Chappell, U.S. Patent No. 5,589,619. The present discovery further contemplates an increase of steroid pathway end products such as Δ^5 sterols and their stanol counterparts with a

decreased accumulation of certain steroid pathway intermediates by also enhancing various specific steroid pathway enzyme activities, such that more of the steroid pathway intermediate compounds are converted to steroid pathway end products.

DNA sequences encoding squalene epoxidases are useful for removal of squalene accumulation, genes encoding sterol methyl transferase I enzymes are useful for removal of cylcoartenol accumulation, genes encoding sterol C4-demethylase are useful for removal of 24-methylene cycloartenol accumulation, genes encoding obtusifoliol C14 α -demethylases are useful for removal of accumulation of obtusifoliol, genes encoding sterol C5-desaturases are useful for removal of stigmasterol-7-enol accumulation, and genes encoding sterol methyl transferase II enzymes are useful for the reduction of accumulated campesterol and concomitant increase of sitosterol.

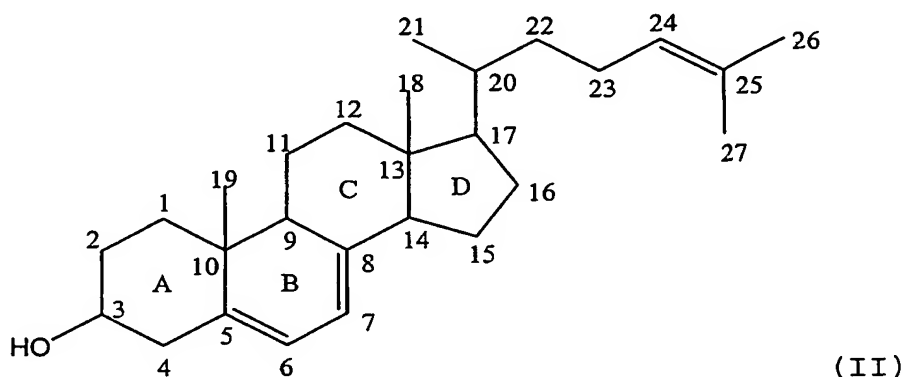
Levels of sitostanol and sitostanol esters can be elevated further by approximately 2- to 40-fold over the transgenic plants of the art having only added genes for HMG CoA reductase by introducing additional genes encoding one or more of the following sterol pathway enzymes: a squalene epoxidase, a sterol methyl transferase I, a sterol C4-demethylase, an obtusifoliol C14 α -demethylase, a sterol C5-desaturase, a sterol methyl transferase II.

As used herein, the term "structural coding sequence" means a DNA sequence which encodes for a peptide, polypeptide, or protein which may be made by a cell following transcription of the DNA to mRNA, followed by translation to the desired peptide, polypeptide, or protein.

The term "sterol" as applied to plants refers to any chiral tetracyclic isopentenoid which may be formed by cyclization of squalene oxide through the transition state possessing stereochemistry similar to the *trans-syn-trans*-

anti-trans-anti configuration, i.e., protosteroid cation, and which retains a polar group at C-3 (hydroxyl or keto), an *all-trans-anti* stereochemistry in the ring system, and a side-chain 20R-configuration (Parker et al. (1992) In Nes et al., Eds., *Regulation of Isopentenoid Metabolism*, ACS Symposium Series No. 497, p. 110; American Chemical Society, Washington, D.C.). The numbering of the carbon atoms of a representative sterol (cholesterol) is shown in the following structure (FORMULA II):

As used herein, the term "sterol" refers to unsaturated hydroxyl group-containing derivatives of a fused, reduced ring system, cyclopenta[α]-phenanthrene, comprising three fused cyclohexane rings (A, B and C) in a phenanthrene arrangement, and a terminal cyclopentane ring (D). The exemplary steroid below (FORMULA II) illustrates the numbering system employed herein in describing the location of groups and substituents.



Sterols may or may not contain a C-5 to C-6 double bond, as this is a feature introduced late in the biosynthetic pathway (note Scheme 1, below). Sterols contain a C₈-C₁₀ side chain at the C-17 position, as shown above.

The term "phytosterol," which applies to sterols found uniquely in plants, refers to a sterol containing a C-5, and in some cases a C-22, double bond. Phytosterols are further

characterized by alkylation of the C-17 side-chain with a methyl or ethyl substituent at the C-24 position. Major phytosterols include, but are not limited to, sitosterol, stigmasterol, campesterol, brassicasterol, etc.

5 Cholesterol, which lacks a C-24 methyl or ethyl side chain, is found in plants but is not unique thereto, and is not a "phytosterol"

"Phytostanols" are saturated forms of phytosterols wherein the C-5 and, when present, C-22 double bond(s)
10 is(are) reduced, and include, but are not limited to, sitostanol, campestanol, and 22-dihydrobrassicastanol.

"Phytosterol esters" and "phytostanol esters" are further characterized by the presence of a fatty acid or phenolic acid moiety rather than a hydroxyl group at the C-3
15 position.

The term "steroid compounds" includes sterols, phytosterols, phytosterol esters, phytostanols, and phytostanol esters.

The term "phytosterol compound" refers to at least one
20 phytosterol, at least one phytosterol ester, or a mixture thereof.

The term "phytostanol compound" refers to at least one phytostanol, at least one phytostanol ester, or a mixture thereof.

25 The term "constitutive promoter" refers to a promoter that operates continuously in a cell, and which is not subject to quantitative regulation. The gene with which such a promoter is associated is always "turned on."

The terms "seed-specific," "fruit-specific," "plastid-specific," etc., as they apply to promoters refer to
30 preferential or exclusive activity of these promoters in these organs or organelles, respectively. "Preferential expression" refers to promoter activity greater in the indicated organs or organelles than elsewhere in the plant.

"Seed-specific" comprehends expression in the aleurone layer, endosperm, and/or embryo of the seed.

As used herein "isolated polynucleotide" means a polynucleotide that is free of one or both of the nucleotide sequences which flank the polynucleotide in the naturally-
5 occurring genome of the organism from which the polynucleotide is derived. The term includes, for example, a polynucleotide or fragment thereof that is incorporated into a vector or expression cassette; into an autonomously
10 replicating plasmid or virus; into the genomic DNA of a prokaryote or eukaryote; or that exists as a separate molecule independent of other polynucleotides. It also includes a recombinant polynucleotide that is part of a hybrid polynucleotide, for example, one encoding a
15 polypeptide sequence.

As used herein "polynucleotide" and "oligonucleotide" are used interchangeably and refer to a polymeric (2 or more monomers) form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. Although
20 nucleotides are usually joined by phosphodiester linkages, the term also includes polymeric nucleotides containing neutral amide backbone linkages composed of aminoethyl glycine units. This term refers only to the primary structure of the molecule. Thus, this term includes double-
25 and single-stranded DNA and RNA. It also includes known types of modifications, for example, labels, methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged
30 linkages (e.g., methyl phosphonates, phosphotriesters, phosphoamidates, carbamates, etc.), those containing pendant moieties, such as, for example, proteins (including for e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), those with intercalators (e.g., acridine,

psoralen, etc.), those containing chelators (e.g., metals, radioactive metals, boron, oxidative metals, etc.), those containing alkylators, those with modified linkages (e.g., alpha anomeric nucleic acids, etc.), as well as unmodified
5 forms of the polynucleotide. Polynucleotides include both sense and antisense strands.

The alternative nucleotide sequences described above are considered to possess substantially similar enzymatic activity to that of the polypeptide-encoding polynucleotide
10 sequences of the present invention if they encode polypeptides having enzymatic activity differing from that of any of the polypeptides encoded by the polynucleotide sequences of the present invention by about 30% or less, preferably by about 20% or less, and more preferably by
15 about 10% or less when assayed by standard enzymatic assays.

As used herein "effective amount" is intended to qualify the amount of an agent which will achieve the goal of a lessening in the severity and/or the frequency of incidence of a disease condition or disorder, over no
20 treatment.

The phrase "steroid pathway products" refers to the products of steroid biosynthesis produced by the action of one or more of squalene epoxidase enzyme, sterol methyl transferase I enzyme, sterol C4-demethylase enzyme,
25 obtusifoliol C14 α -demethylase enzyme, sterol C5-desaturase enzyme, and sterol methyl transferase II enzyme. Specific examples of steroid pathway products include, but are not limited to, sitosterol, sitostanol, stigmasterol and stigmastanol.

30 In the context of the present disclosure, a "non-transformed" plant or cell refers to a plant or cells which does not comprise introduced polynucleotides encoding a polypeptide having 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity and at least one polypeptide

having squalene epoxidase enzyme activity, sterol methyl transferase I enzyme activity, sterol C4-demethylase enzyme activity, obtusifoliol C14 α -demethylase enzyme activity, sterol C5-desaturase enzyme activity, or sterol methyl transferase II enzyme activity. Thus, a plant or cell that contains introduced polynucleotide sequences other than those above, would still be considered "non-transformed."

As used herein, "peptide" and "protein" are used interchangeably and mean a compound that consists of two or more amino acids that are linked by means of peptide bonds.

I. Plant Steroid Biosynthesis

To aid the reader in understanding the present invention, descriptions of the sterol compound biosynthetic pathway are presented below. These descriptions identify enzymes useful in achieving the modifications to the biosynthesis and accumulation of sterol compounds described herein, and identify sources of nucleic acid sequences encoding these enzymes.

Various steps in the steroid compound biosynthetic pathway in plants are shown in Scheme 1, below. The numbers over the arrows refer to plant sterol compound biosynthetic pathway enzymes and genes as indicated in Table 1.

SCHEME 1

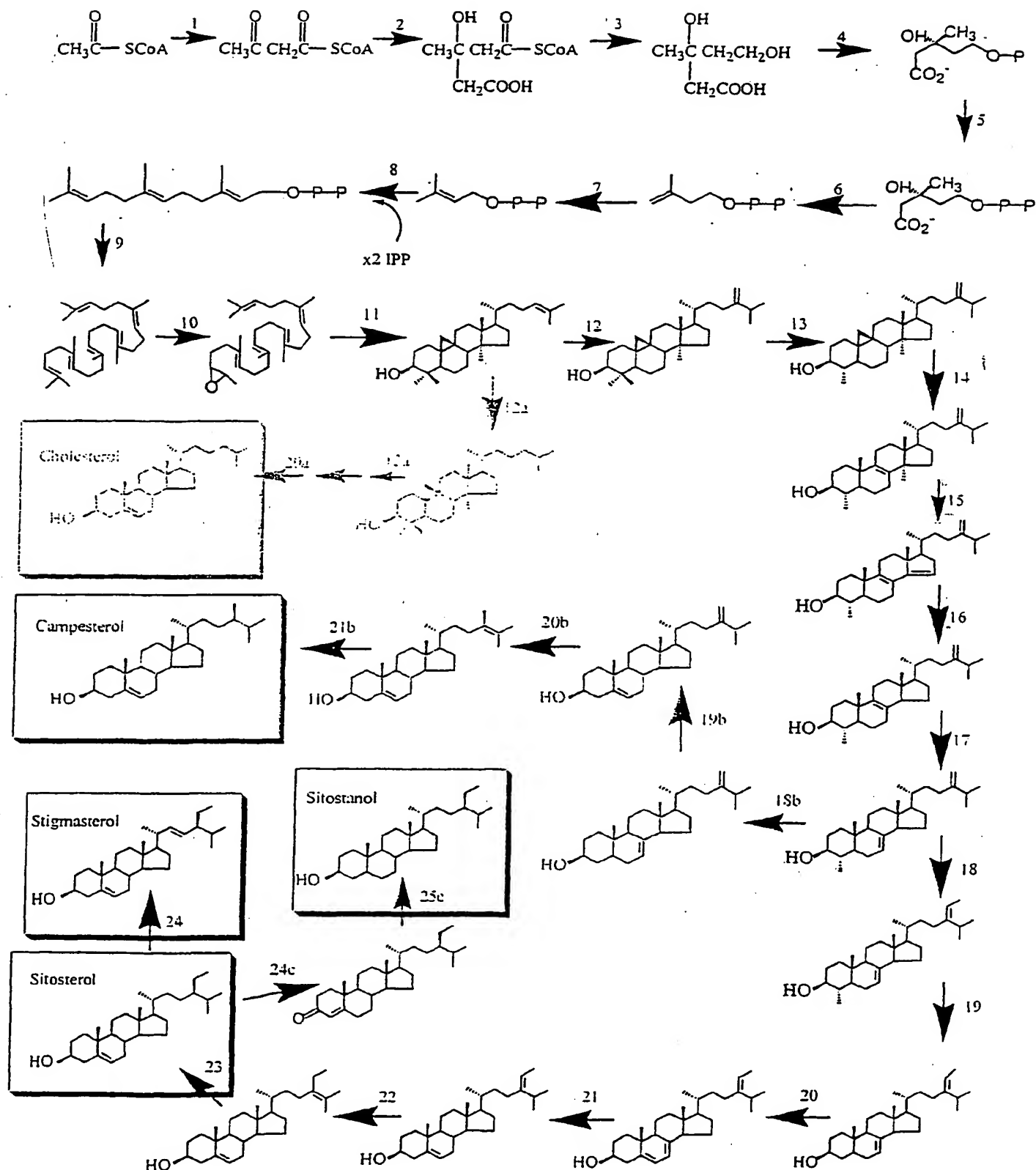


Table 1

Plant Sterol Compound Pathway Enzymes and Genes

Enzyme	Step in Pathway	GenBank Gene ID
Acetoacetyl-CoA thiolase	1	X78116
HMG-CoA synthase	2	X83882
HMG-CoA reductase	3	X15032
		L19262
Mevalonate kinase	4	X77793
Phosphomevalonate kinase	5	Not available
Mevalonate pyrophosphate decarboxylase	6	Y14325
Isopentenyl diphosphate isomerase	7	U49259
		U47324
Farnesyl pyrophosphate synthase	8	X75789
Squalene synthase	9	AF0045 60
Squalene epoxidase	10	AB0168 83
Squalene cyclase	11	U87266
Sterol C-24 methyltransferase	12, 18	U71400
Sterol C-4 demethylase	13, 19	Not available
Cycloeucalenol- obtusifolliol isomerase	14	Not available
Sterol C-14 demethylase	15	U74319
Sterol C-14 reductase	16	PCT WO

		97/48793
Sterol C-8 isomerase	17	AF0303
		57
Sterol C-5 desaturase	20	X90454
Sterol C-7 reductase	21	U49398
Sterol C-24 isomerase	22	Klahre
		et al.
		(1998)
		<i>Plant Cell</i>
		10: 1677-
		1690
Sterol C-24 reductase	23	Same
		as 22
Sterol C-22 desaturase	24	Not
		available
Sterol C-5 reductase	25	WO
		00/61771

The plant sterol compound biosynthesis pathway has two distinct components. The early pathway reactions, leading from acetyl-CoA to squalene via mevalonic acid, are common to other isoprenoids. The later pathway reactions, leading from squalene to the major plant sterol compounds such as sitosterol, campesterol and stigmasterol, are committed biosynthetic reactions.

The early pathway reactions have been studied in fungi and plants (Lees et al., *Biochemistry and Function of Sterols*, Nes and Parish, Eds., CRC Press, 85-99 (1997); Newman and Chappell, *Biochemistry and Function of Sterols*, Nes and Parish, Eds., CRC Press, 123-134 (1997); Bach et al., *Biochemistry and Function of Sterols*, Nes and Parish, Eds., CRC Press, 135-150 (1997)).

Acetoacetyl CoA thiolase (EC 2.3.1.9) catalyzes the first reported reaction, which consists of the formation of acetoacetyl CoA from two molecules of acetyl CoA (Dixon et al., *J. Steroid Biochem. Mol. Biol.* 62: 165-171 (1997)).

5 This enzyme has been purified from radish. A radish cDNA has been isolated by functional complementation in *Saccharomyces cerevisiae* (GeneBank Accession # X78116). A radish cDNA has also been screened against a cDNA library of *Arabidopsis thaliana* (Vollack and Bach, *Plant Physiology* 10 111: 1097-1107 (1996)).

HMGCoA synthase (EC 4.1.3.5) catalyzes the production of HMGCoA. This reaction condenses acetyl CoA with acetoacetyl CoA to yield HMGCoA. HMGCoA synthase has been purified from yeast. A plant HMGCoA synthase cDNA has also 15 been isolated from *Arabidopsis thaliana* (Montamat et al., *Gene* 167: 197-201 (1995)).

HMGCoA reductase, also referred to as 3-hydroxy-3-methylglutaryl-coenzyme A (EC 1.1.1.34), catalyzes the reductive conversion of HMGCoA to mevalonic acid (MVA). 20 This reaction is reported to play a role in controlling plant isoprenoid biosynthesis (Gray, *Adv. Bot. Res.* 14: 25-91 (1987); Bach et al., *Lipids* 26: 637-648 (1991); Stermer et al., *J. Lipid Res.* 35: 1133-1140 (1994). Plant HMGCoA reductase genes are often encoded by multigene families. 25 The number of genes comprising each multigene family varies, depending on the species, ranging from two in *Arabidopsis thaliana* to at least seven in potato. Overexpression of plant HMGCoA reductase genes in transgenic tobacco plants has been reported to result in the overproduction of 30 phytosterols (Schaller et al., *Plant Physiol.* 109: 761-770 (1995)).

Mevalonate kinase (EC 2.7.1.36) catalyzes the phosphorylation of mevalonate to produce mevalonate 5-phosphate. It has been reported that mevalonate kinase

plays a role in the control of isoprenoid biosynthesis (Lalitha et al., *Indian. J. Biochem. Biophys.* 23: 249-253 (1986)). A mevalonate kinase gene from *Arabidopsis thaliana* has been cloned (GeneBank accession number X77793; Riou et al., *Gene* 148: 293-297 (1994)).

Phosphomevalonate kinase (EC 2.7.4.2) (MVAP kinase) is an enzyme associated with isoprene and ergosterol biosynthesis that converts mevalonate-5-phosphate to mevalonate-5-pyrophosphate utilizing ATP (Tsay et al., *Mol. Cell. Biol.* 11: 620-631 (1991)).

Mevalonate pyrophosphate decarboxylase ("MVAPP decarboxylase") (EC 4.1.1.33) catalyzes the conversion of mevalonate pyrophosphate to isopentenyl diphosphate ("IPP"). The reaction is reported to be a decarboxylation/dehydration reaction which hydrolyzes ATP and requires Mg^{2+} . A cDNA encoding *Arabidopsis thaliana* MVAPP decarboxylase has been isolated (Toth et al., *J. Biol. Chem.* 271: 7895-7898 (1996)). An isolated *Arabidopsis thaliana* MVAPP decarboxylase gene was reported to be able to complement the yeast MVAPP decarboxylase.

Isopentenyl diphosphate isomerase ("IPP:DMAPP") (EC 5.3.3.2) catalyzes the formation of dimethylallyl pyrophosphate (DMAPP) from isopentenyl pyrophosphate (IPP). Plant IPP:DMAPP isomerase gene sequences have been reported for this enzyme. It has also been reported that IPP:DMAPP isomerase is involved in rubber biosynthesis in a latex extract from *Hevea* (Tangpakdee et al., *Phytochemistry* 45: 261-267 (1997)).

Farnesyl pyrophosphate synthase (EC 2.5.1.1) is a prenyltransferase which has been reported to play a role in providing polyisoprenoids for sterol compound biosynthesis as well as a number of other pathways (Li et al., *Gene* 17: 193-196 (1996)). Farnesyl pyrophosphate synthase combines DMAPP with IPP to yield geranyl pyrophosphate ("GPP"). The

same enzyme condenses GPP with a second molecule of IPP to produce farnesyl pyrophosphate ("FPP"). FPP is a molecule that can proceed down the pathway to sterol compound synthesis, or that can be shuttled through other pathways leading to the synthesis of quinones or sesquiterpenes.

Squalene synthase (EC 2.5.1.21) reductively condenses two molecules of FPP in the presence of Mg^{2+} and NADPH to form squalene. The reaction involves a head-to-head condensation, and forms a stable intermediate, presqualene diphosphate. The enzyme is subject to sterol demand regulation similar to that of HMGCoA reductase. The activity of squalene synthase has been reported to have a regulatory effect on the incorporation of FPP into sterol and other compounds for which it serves as a precursor (Devarenne et al., *Arch. Biochem. Biophys.* 349: 205-215 (1998)).

Squalene epoxidase (EC 1.14.99.7) (also called squalene monooxygenase) catalyzes the conversion of squalene to squalene epoxide (2,3-oxidosqualene), a precursor to the initial sterol molecule in the sterol compound biosynthetic pathway, cycloartenol. This is the first reported step in the pathway where oxygen is required for activity. The formation of squalene epoxide is also the last common reported step in sterol biosynthesis of animals, fungi, and plants.

The later pathway of sterol compound biosynthetic steps starts with the cyclization of squalene epoxide and ends with the formation of 5 -24-alkyl sterols in plants.

2,3-oxidosqualene cycloartenol cyclase (EC 5.4.99.8) (also called cycloartenol synthase) is the first step in the sterol compound pathway that is plant-specific. The cyclization of 2,3-oxidosqualene leads to lanosterol in animals and fungi, while in plants the product is cycloartenol. Cycloartenol contains a 9,19-cyclopropyl

ring. The cyclization is reported to proceed from the epoxy end in a chair-boat-chair-boat sequence that is mediated by a transient C-20 carbocationic intermediate.

S-adenosyl-L-methionine:sterol C-24 methyl transferase ("SMT1") (EC 2.1.1.41) catalyzes the transfer of a methyl group from S-adenosyl-L-methionine to the C-24 center of the sterol side chain (Nes et al. (1991) *J. Biol. Chem.* 266(23):15202-15212). This is the first of two methyl transfer reactions that have been reported to be an obligatory and rate-limiting step of the sterol compound-producing pathway in plants. The second methyl transfer reaction occurs later in the pathway after the Δ^{8-7} isomerase. The enzyme responsible for the second methyl transfer reaction is named SMTII (Bouvier-Nave, P. et al., (1997) *Eur. J. Biochem.*, 246: 518-529). An isoform, SMTII, catalyzes the conversion of cycloartenol to a $\Delta^{23(24)}$ -24-alkyl sterol, cyclosadol (Guo et al. (1996) *Tetrahed. Lett.* 37(38):6823-6826).

Sterol C-4 demethylase catalyzes the first of several demethylation reactions, which results in the removal of the two methyl groups at C-4. While in animals and fungi the removal of the two C-4 methyl groups occurs consecutively, in plants it has been reported that there are other steps between the first and second C-4 demethylations. The C-4 demethylation is catalyzed by a complex of microsomal enzymes consisting of a monooxygenase, an NAD⁺-dependent sterol 4-decarboxylase, and an NADPH-dependent 3-ketosteroid reductase.

Cycloeucalenol-obtusifoliol isomerase ("COI") catalyzes the opening of the cyclopropyl ring at C-9. The opening of the cyclopropyl ring at C-9 creates a double bond at C-8.

Sterol C-14 demethylase catalyzes demethylation at C-14, which removes the methyl group at C-14 and creates a double bond at that position. In both fungi and animals,

this is the first step in the sterol synthesis pathway. Sterol 14-demethylation is mediated by a cytochrome P-450 complex.

Sterol C-14 reductase catalyzes a C-14 demethylation
5 that results in the formation of a double bond at C-14 (Ellis et al., *Gen. Microbiol.* 137: 2627-2630 (1991)). This double bond is removed by a Δ^{14} reductase. The normal substrate is 4-methyl-8,14,24 (24^1)-trien- 3β -ol. NADPH is the normal reductant.

10 Sterol C-8 isomerase catalyzes a reaction that involves further modification of the tetracyclic rings or the side chain (Duratti et al., *Biochem. Pharmacol.* 34: 2765-2777 (1985)). The kinetics of the sterol isomerase-catalyzed reaction favor a Δ^8 Δ^7 isomerase reaction that produces a
15 Δ^7 group.

Sterol C-5 desaturase catalyzes the insertion of the Δ^5 -double bond that normally occurs at the Δ^7 -sterol level, thereby forming a $\Delta^{5,7}$ -sterol (Parks et al., *Lipids* 30: 227-230 (1995)). The reaction has been reported to involve the
20 stereospecific removal of the 5α and 6α hydrogen atoms, biosynthetically derived from the 4 pro-R and 5 pro-S hydrogens of the (+) and (-) R-mevalonic acid, respectively. The reaction is obligatorily aerobic, and requires NADPH or NADH. The desaturase has been reported to be a multienzyme
25 complex present in microsomes. It consists of the desaturase itself, cytochrome b_5 , and a pyridine nucleotide-dependent flavoprotein. The Δ^5 -desaturase is reported to be a mono-oxygenase that utilizes electrons derived from a reduced pyridine nucleotide via cytochrome b_5 .

30 Sterol C-7 reductase catalyzes the reduction of a Δ^7 -double bond in $\Delta^{5,7}$ -sterols to generate the corresponding Δ^5 -sterol. It has been reported that the mechanism involves,

like many other sterol enzymes, the formation of a carbocationic intermediate via 'electrophilic "attack" by a proton.

Sterol C-24(28) isomerase catalyzes the reduction of a
5 $\Delta^{24(28)}-\Delta^{24}$, a conversion that modifies the side chain. The product is a $\Delta^{24(25)}$ -24-alkyl sterol. Sterol C-24 reductase catalyzes the reduction of the $^{24(25)}$ double bond at C-24, which produces sitosterol. Recently, Klahre et al. ((1998) *Plant Cell* 10:1677-1690) discovered that both the
10 isomerization and reduction steps are catalyzed by an enzyme coded by the same gene, i.e., DIM/DWF1.

Sterol C-22 desaturase (EC 2.7.3.9) catalyzes the formation of a double bond at C-22 on the side chain. This formation of a double bond at C-22 on the side chain marks
15 the end of the sterol compound biosynthetic pathway, and results in the formation of stigmasterol (Benveniste (1986) *Annu. Rev. Plant Physiol.* 37:275-308). The C-22 desaturase in yeast, which is the reported final step in the biosynthesis of ergosterol in that organism, requires NADPH
20 and molecular oxygen. In addition, the reaction is also reported to involve a cytochrome P450 that is distinct from a cytochrome P450 participating in demethylation reactions (Lees et al. (1995) *Lipids* 30: 221-226).

Phytosterols are biogenetic precursors of
25 brassinosteroids, steroid alkaloids, steroid sapogenins, ecdysteroids, and steroid hormones. This precursor role of phytosterols is often described as a "metabolic" function. A common transformation of free sterols in tissues of vascular plants is the conjugation at the 3-hydroxy group of
30 sterols with long-chain fatty acids to form steryl esters, or with a sugar, usually with a single molecule of β -D-glucose, to form steryl glycosides. Some of the steryl glycosides are additionally esterified, at the 6-hydroxy

group of the sugar moiety, with long-chain fatty acids to form acylated steryl glycosides.

The existence of several enzymes that are specifically associated with the synthesis and breakdown of conjugated sterols has been reported (Wojciechowski, *Physiology and Biochemistry of Sterols*, eds. Patterson, Nes, AOCS Press, 361 (1991)). Enzymes involved in this process include: UDPGlc:Sterol glucosyltransferase, phospho(galacto)glyceride steryl glucoside acyltransferase, and sterylglycoside and sterylester hydrolases.

UDPGlc:sterol glucosyltransferase (EC 2.4.1.173) catalyzes glucosylation of phytosterols by glucose transfer from UDP-glucose ("UDPGl"). The formation of steryl glycosides can be measured using UDP-[¹⁴C]glucose as the substrate. Despite certain differences in their specificity patterns, all reported UDPGlc:sterol glucosyltransferases preferentially glucosylate only sterols or sterol-like molecules that contain a C-3 hydroxy group, a β -configuration, and which exhibit a planar ring. It has been reported that UDPGlc:sterol glucosyltransferases are localized in the microsomes.

Phospho(galacto)glyceride steryl glucoside acyltransferase catalyzes the formation of acylated steryl glycosides from the substrate steryl glycoside by transfer of acyl groups from some membranous polar acyllipids to steryl glycoside molecules.

Acylglycerol:sterol acyltransferase (EC 2.3.1.26) catalyzes the reaction wherein certain acylglycerols act as acyl donors in a phytosterol esterification. In plants, the activity of acylglycerol:sterol acyltransferase is reported to be associated with membranous fractions. A pronounced specificity for shorter chain unsaturated fatty acids was reported for all acyltransferase preparations studied in plants. For example, acylglycerol:sterol acyltransferases

from spinach leaves and mustard roots can esterify a number of phytosterols.

Sterylglycoside and sterylester hydrolases ("SG-hydrolases") catalyze the enzymatic hydrolysis of
5 sterylglycosides to form free sterols. The SG-hydrolase activity is not found in mature, ungerminated seeds, is reported to emerge only after the third day of germination, and is found mainly in the cotyledons. It has been reported that phospho(galacto)glyceride:SG acyltransferase may
10 catalyze a reversible reaction. Enzymatic hydrolysis of sterylesters in germinating seeds of mustard, barley and corn is reported to be low in dormant seeds, but increases during the first ten days of germination. This activity is consistent with a decrease in sterylesters and an increase
15 in free sterols over the same temporal period.

II. Processes for Modifying Steroid Compound Biosynthesis and Accumulation

In order to obtain seed producing oil containing
20 elevated levels of phytosterols and phytosterol esters such as sitosterol and sitosterol esters, these recombinant constructs or expression cassettes can be introduced into plant cells by any number of conventional means known in the art and regenerated into fertile transgenic plants. The
25 genome of such plants can then comprise introduced DNA encoding various steroid pathway enzymes, alone or in combination, that achieves the desirable effect of enhancing the levels of phytosterols, phytosterol esters, mixtures thereof in the oil of seed thereof.

30 Preferably, the genome can comprise introduced DNA encoding a HMG CoA reductase enzyme and an introduced DNA encoding one or more of a squalene epoxidase, a sterol methyl transferase I, a sterol C4-demethylase, an obtusifoliol C14 α -demethylase, a sterol C5-desaturase, a

sterol methyl transferase II. In each case, the foregoing introduced DNAs can be operatively linked to regulatory signals that cause seed-specific expression thereof.

The present invention encompasses not only such
5 transgenic plants, but also transformed plant cells, including cells and seed of such plants, as well as progeny of such plants, for example produced from the seed. Transformed plant cells and cells of the transgenic plants encompassed herein can be grown in culture for a time and
10 under appropriate conditions to produce oil containing elevated levels of phytosterols and/or phytostanols and their corresponding esters. Alternatively, the phytosterols, phytostanols, and their corresponding esters can be isolated directly from the cultures.

15 In addition, of course, seed obtained from the transgenic, progeny, hybrid, etc., plants disclosed herein can be used in methods for obtaining oil containing phytosterols, phytosterol esters, phytostanols, phytostanol esters, or mixtures thereof employing extraction and
20 processing procedures known in the art. Note, in this regard, Kochhar (1983) *Prog. Lipid Res.* 22: 161-188.

The present invention also encompasses a method of producing a plant that accumulates an elevated level of sitosterol, at least one sitosterol ester, sitostanol, at
25 least one sitostanol ester, or mixtures thereof, in seeds thereof compared to seeds of a corresponding plant comprising no introduced DNA encoding a polypeptide or protein that affects the biosynthesis of sterols, phytosterols, phytosterol esters, phytostanols, phytostanol
30 esters, or combinations thereof, comprising sexually crossing a transgenic plant of the present invention with such a corresponding plant. The latter can be a non-transgenic plant, or a transgenic plant containing introduced DNA encoding a trait other than one affecting

sterol, phytosterol, etc., biosynthesis. For example, such trait may be insect or herbicide resistance. Plants produced by this method also form part of the present invention.

5 Also included are plants that accumulate an elevated level of sitosterol, at least one sitosterol ester, sitostanol, at least one sitostanol ester, or mixtures thereof, in seeds thereof compared to seeds of a corresponding plant comprising no introduced DNA encoding a polypeptide or protein that affects the biosynthesis of
10 sterols, phytosterols, phytosterol esters, phytostanols, phytostanol esters, or combinations thereof, which are apomictic.

 A process of increasing the formation of steroid
15 pathway products in a transformed host cell as compared to an otherwise identical non-transformed host cell comprising the following steps. A host cell is transformed with a recombinant vector comprising (a) as operably linked components in the 5' to 3' direction, a promoter, a DNA
20 sequence encoding a polypeptide exhibiting 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity, and a transcription termination signal sequence; and (b) as operably linked components in the 5' to 3' direction, a promoter, a DNA sequence encoding a steroid pathway enzyme,
25 and a transcription termination signal sequence. The steroid pathway enzyme is a squalene epoxidase enzyme, a sterol methyl transferase I enzyme, a sterol C4-demethylase enzyme, a obtusifoliol C14 α -demethylase enzyme, a sterol C5-desaturase enzyme, and a sterol methyl transferase II
30 enzyme. The transformed plant cell is regenerated into a transgenic plant.

 A plant contemplated by this invention is a vascular, multicellular higher plant. Such higher plants will hereinafter be usually referred to simply as "plants". Such

"plants" include both complete entities having leaves, stems, seeds, roots and the like as well as callus and cell cultures that are monocotyledonous and dicotyledonous. Dicotyledonous plants are a preferred embodiment of the present invention.

Preferred plants are members of the Solanaceae, Leguminosae, Ammiaceae, Brassicaceae, Gramineae, Carduaceae and Malvaceae families. Exemplary plant members of those families are tobacco, petunia and tomato (Solanaceae), soybean and alfalfa (Leguminosae), carrot (Ammiaceae), corn, maize and barley (Gramineae), *Arabidopsis* (Brassicaceae), guayule (Carduaceae), and cotton (Malvaceae). A preferred plant is tobacco of the strain *Nicotiana tabacum* (N. *Tabacum*), cotton of the strain Coker line 312-5A, soybean of the strain *Glycine max*, alfalfa of the strain RYSI or tomato of the strain *Lycopersicon esculentum*. Other plants include canola, maize and rape.

A transgenic plant contemplated by this invention is produced by transforming a plant cell or protoplast with an added, exogenous structural gene that encodes a polypeptide having HMG-CoA reductase activity and an exogenous structural gene that encodes at least one polypeptide having steroid pathway enzyme activity to produce a transformed plant cell, and regenerating a transgenic plant form the transformed plant cell. The encoded polypeptide is expressed both in the transformed plant cell or protoplast and the resulting transgenic plant. (The phrase "plant cell" will hereinafter be used to include a plant protoplast, except where plant protoplasts are specifically discussed).

A non-transgenic plant that serves as the source of the plant cell that is transformed, i.e. the precursor cell, is referred to herein as a "native, non-transgenic" plant. The

native, non-transgenic plant is of the same strain as the formed transgenic plant.

Sterol production in a transgenic plant of the present invention is increased by increasing the activity of the enzyme HMG-CoA reductase, which enzyme catalyzes the conversion of 3-hydroxy-3-methylglutaryl Coenzyme A (HMG-CoA) to mevalonate and the activity of at least one other steroid pathway enzyme. As used herein, the term "specific activity" means the activity normalized to cellular protein content.

HMG-CoA reductase activity is increased by increasing the amount (copy number) of a gene encoding a polypeptide having HMG-CoA reductase catalytic activity. Expression of the increased amount of that encoded structural gene enhances the activity of that enzyme.

The amount of the expressed gene is increased by transforming a plant cell with a recombinant DNA molecule comprising a vector operatively linked to a DNA segment that encodes a polypeptide having HMG-CoA reductase activity, and a promoter suitable for driving the expression of that polypeptide in that plant cell, and culturing the transformed plant cell into a transgenic plant. Such a polypeptide includes intact as well as a catalytically active, truncated HMG-CoA reductase proteins.

Thus, a transformed plant cell and a transgenic plant have one or more added, exogenous genes that encode a polypeptide having HMG-CoA reductase activity and at least one other steroid pathway enzyme activity relative to a native, non-transgenic plant or untransformed plant cell of the same type. As such, a transformed plant cell or transgenic plant can be distinguished from an untransformed plant cell or native, nontransgenic plant by standard technology such as agarose separation of DNA fragments or mRNAs followed by transfer and appropriate blotting with DNA

or RNA, e.g., Southern or Northern blotting, or by use of polymerase chain reaction technology, as are well known. Relative HMG-CoA reductase activity of the transformed cell or transgenic plant with untransformed cells and native, 5 non-transgenic plants or cell cultures therefrom can also be compared, with a relative activity for that enzyme of about 1.5:1 for transgenic (transformed) to native (untransformed) showing transformation. Higher relative activity ratios such as about 15:1 have also been observed.

10 Sterol accumulation can also be used to distinguish between native, non-transgenic and transgenic plants. A transgenic plant has at least about twice the total sterol content as a native, non-transgenic plant where a single added gene is present. Greater differences up to about 15 forty-fold have also been observed.

Sitostanol, sitostanol ester, and tocopherol biosynthesis and accumulation in plants can be modified in accordance with the present invention by variously expressing the nucleic acid coding sequences discussed 20 above, alone or in combination, as described herein. The expression of sequences encoding sterol methyltransferase II enzymes facilitates the production of plants in which the biosynthesis and accumulation of campesterol, campestanol, and their esters can be reduced as these enzymes shunt 25 sterol intermediates away from campesterol, and toward sitosterol and sitostanol.

III. DNA Encoding Useful Polypeptides

The present invention contemplates a recombinant 30 construct or a recombinant vector that contains a DNA sequence encoding a polypeptide exhibiting 3-hydroxy-3-methylglutaryl-Coenzyme A (HMG-CoA) reductase activity and a DNA sequence encoding a polypeptide exhibiting the activity of a steroid pathway enzyme. Each polypeptide-encoding DNA

sequence is operably linked in the 5' to 3' direction independent of the other sequence. Each DNA sequence in the 5' to 3' direction comprises a promoter, then the DNA sequence encoding the polypeptide then a transcription termination signal sequence. The steroid pathway enzyme is a squalene epoxidase enzyme, a sterol methyl transferase I enzyme, a sterol C4-demethylase enzyme, a obtusifolioside C14 α -demethylase enzyme, a sterol C5-desaturase enzyme, or a sterol methyl transferase II enzyme. It is contemplated that HMG-CoA reductase and steroid pathway enzyme activities come from a mutant or truncated form of those enzymes, such as a truncated HMG-CoA reductase lacking the transmembrane region while retaining a functional catalytic domain. Several HMG CoA reductase sequences are known in the art. An amino acid alignment for these is shown in FIG. 32. The sources of the sequences used in building the multiple alignment are listed in Table 5.

Table 5. Sources of Sequences Used In Building The Multiple Alignment

methanobac	swissprot:hmdh_meth	Begin:1	End:397	O26662 methanobacterium thermoautotrophicur
methanococ	swissprot:hmdh_metja	Begin:1	End:405	Q58116 methanococcus jannaschii. 3-hydroxy-3
halobacter	swissprot:hmdh_halvo	Begin:1	End:403	Q59468 halobacterium volcanii (haloferax volcar
sulfolobus	swissprot:hmdh_sulso	Begin:1	End:409	O08424 sulfolobus solfataricus. 3-hydroxy-3-me
yeast2	gp_pln1:yschmgcr2_1	Begin:1	End:1045	M22255 Saccharomyces cerevisiae Yeast HMG
yeast1	gp_pln1:yschmgcr1_1	Begin:1	End:1054	M22002 Saccharomyces cerevisiae Yeast HMG
phycomyces	swissprot:hmdh_phybl	Begin:1	End:105	Q12649 phycomyces blakesleeana. 3-hydroxy-
fusarium	swissprot:hmdh_fusmo	Begin:1	End:976	Q12577 fusarium moniliforme (gibberella fujikurc
candida	gp_pln1:ab012603_1	Begin:1	End:934	AB012603 Candida utilis Candida utilis HMG mF
dictyoste2	swissprot:hmd2_dicdi	Begin:1	End:481	P34136 dictyostelium discoideum (slime mold). :
wheat1	pir2:pq0761	Begin:1	End:150	hydroxymethylglutaryl-CoA reductase (NADPH)
rice	swissprot:hmdh_orysa	Begin:1	End:509	P48019 oryza sativa (rice). 3-hydroxy-3-methylg
corn	sp_plant:o24594	Begin:1	End:579	O24594 zea mays (maize). 3-hydroxy-3-methylg
wheat3	pir2:pq0763	Begin:1	End:150	hydroxymethylglutaryl-CoA reductase (NADPH)
wheat2	pir2:pq0762	Begin:1	End:150	hydroxymethylglutaryl-CoA reductase (NADPH)
soybean	gmbx6:30820_1r59f1	Begin:101	End:259	from proprietary soy sequence database
rubbertre3	swissprot:hmd3_hevbr	Begin:1	End:586	Q00583 hevea brasiliensis (para rubber tree). 3-
rosyperiwi	swissprot:hmdh_catro	Begin:1	End:601	Q03163 catharanthus roseus (rosy periwinkle) (r
tomato	swissprot:hmd2_lyces	Begin:1	End:602	P48022 lycopersicon esculentum (tomato). 3-hy
woodtobacc	swissprot:hmdh_nicsy	Begin:1	End:604	Q01559 nicotiana glauca (wood tobacco). 3-h
potato	gp_pln1:pothmgri_1	Begin:1	End:596	L01400 Solanum tuberosum Potato hydroxymeth
radish	sp_plant:q43826	Begin:1	End:573	Q43826 raphanus sativus (radish). hydroxymeth
arabidopsis1	gp_pln1:athhmgcoa_1	Begin:1	End:592	L19261 Arabidopsis thaliana Arabidopsis thalian
cucumismel	gp_pln1:ab021862_1	Begin:1	End:587	AB021862 Cucumis melo Cucumis melo mRNA
rubbertre2	swissprot:hmd2_hevbr	Begin:1	End:210	P29058 hevea brasiliensis (para rubber tree). 3-
rubbertre1	swissprot:hmd1_hevbr	Begin:1	End:575	P29057 hevea brasiliensis (para rubber tree). 3-
camptothec	swissprot:hmdh_camac	Begin:1	End:593	P48021 camptotheca acuminata. 3-hydroxy-3-m
arabidops2	swissprot:hmd2_arath	Begin:1	End:562	P43256 arabidopsis thaliana (mouse-ear cress). :
chineseham	swissprot:hmdh_crigr	Begin:1	End:887	P00347 cricetus griseus (chinese hamster). 3-
chineseha2	gp_rod:cruhmg14_1	Begin:1	End:887	L00183 Cricetus sp. Hamster 3-hydroxy-3-met
syrianhamst	gp_rod:hamhmgcob_1	Begin:1	End:887	M12705 Mesocricetus auratus Syrian hamster 3-
rat	swissprot:hmdh_rat	Begin:1	End:887	P51639 rattus norvegicus (rat). 3-hydroxy-3-met
rabbit	swissprot:hmdh_rabit	Begin:1	End:888	Q29512 oryctolagus cuniculus (rabbit). 3-hydrox
human	gp_pri2:humhmgcoa_1	Begin:1	End:888	M11058 Homo sapiens Human 3-hydroxy-3-met
mouse	gp_rod:mushmgcoa_1	Begin:1	End:224	M62766 Mus musculus Mouse HMG-CoA reduc
xenopus	swissprot:hmdh_xenla	Begin:1	End:883	P20715 xenopus laevis (african clawed frog). 3-
seaurchin	swissprot:hmdh_strpu	Begin:1	End:932	P16393 strongylocentrotus purpuratus (purple s
cockroach	swissprot:hmdh_blage	Begin:1	End:856	P54960 blattella germanica (german cockroach)
drosophila	swissprot:hmdh_drome	Begin:1	End:916	P14773 drosophila melanogaster (fruit fly). 3-hyc
dictyoste1	swissprot:hmd1_dicdi	Begin:1	End:552	P34135 dictyostelium discoideum (slime mold). :
schistosom	swissprot:hmdh_schma	Begin:1	End:948	P16237 schistosoma mansoni (blood fluke). 3-hy
archaeoglo	swissprot:hmdh_arcbu	Begin:1	End:436	O28538 archaeoglobus fulgidus. 3-hydroxy-3-mi
pseudomonas	gp_bct1:psehmgcoa_1	Begin:1	End:428	M24015 Pseudomonas mevalonii P.mevalonii HI

5

These sequences, and their truncated counterparts, are useful in the present invention. Examples of such preferred HMG CoA reductases include the truncated rubber and *Arabidopsis* HMG CoA reductases disclosed herein.

10

Other enzyme-encoding DNAs can be introduced into plants to elevate even further the levels of desirable $\Delta 5$ sterols and their reduced stanol counterparts as well as other phytosterols and tocopherols. Thus, the DNA sequences contemplated for use in the present invention, which can be

15

used alone or in various combinations as discussed below,

include, but are not limited to, those encoding the following enzymes: 3-hydroxysteroid oxidases; steroid 5-reductases; sterol methyltransferases; sterol acyltransferases; and S-adenosylmethionine-dependent α -tocopherol methyltransferases.

In each case, the sequences encoding these enzymes can comprise an expression cassette comprising, operably linked in the 5' to 3' direction, a seed-specific promoter, the enzyme coding sequence, and a transcriptional termination signal sequence functional in a plant cell such that the enzyme is successfully expressed. For use in the methods disclosed herein, the recombinant constructs or expression cassettes can be incorporated in a vector, for example a plant expression vector. Such vectors can be transformed into host cells such as bacterial cells, for example during the preparation or modification of the recombinant constructs, and plant cells. Thus, the invention encompasses plants and seeds comprising such transformed plant cells.

It will be apparent to those of skill in the art that the nucleic acid sequences set forth herein, either explicitly, as in the case of the sequences set forth above, or implicitly with respect to nucleic acid sequences generally known and not present herein, can be modified due to the built-in redundancy of the genetic code and noncritical areas of the polypeptide that are subject to modification and alteration. In this regard, the present invention contemplates allelic variants of structural genes encoding a polypeptide having HMG-CoA reductase activity.

The previously described DNA segments are noted as having a minimal length, as well as total overall length. That minimal length defines the length of a DNA segment having a sequence that encodes a particular polypeptide having HMG-CoA reductase activity. As is well known in the

art, as long as the required DNA sequence is present (including start and stop signals), additional base pairs can be present at either end of the segment and that segment can still be utilized to express the protein. This, of course, presumes the absence in the segment of an operatively linked DNA sequence that represses expression, expresses a further product that consumes the enzyme desired to be expressed, expresses a product other than the desired enzyme or otherwise interferes with the structural gene of the DNA segment.

Thus, as long as the DNA segment is free of such interfering DNA sequences, a DNA segment of the invention can be up to 15,000 base pairs in length. The maximum size of a recombinant DNA molecule, particularly a plant integrating vector, is governed mostly by convenience and the vector size that can be accommodated by a host cell, once all of the minimal DNA sequences required for replication and expression, when desired, are present. Minimal vector sizes are well known.

Also encompassed by the present invention are nucleotide sequences biologically functionally equivalent to those disclosed herein, that encode conservative amino acid changes within the amino acid sequences of the presently disclosed enzymes, producing "silent" changes therein. Such nucleotide sequences contain corresponding base substitutions based upon the genetic code compared to the nucleotide sequences encoding the presently disclosed enzymes. Substitutes for an amino acid within the enzyme sequences disclosed herein is selected from other members of the class to which the naturally occurring amino acid belongs. Amino acids can be divided into the following four groups: (1) acidic amino acids; (2) basic amino acids; (3) neutral polar amino acids; and (4) neutral non-polar amino acids. Representative amino acids within these various

groups include, but are not limited to: (1) acidic (negatively charged) amino acids such as aspartic acid and glutamic acid; (2) basic (positively charged) amino acids such as arginine, histidine, and lysine; (3) neutral polar amino acids such as glycine, serine, threonine, cysteine, cystine, tyrosine, asparagine, and glutamine; and (4) neutral nonpolar (hydrophobic) amino acids such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine.

10

A. HMG-CoA Reductase

The introduction of an HMG CoA reductase gene into a cell results in a higher carbon throughput through the steroid synthesis pathway. The introduction of a truncated HMG CoA reductase gene (lacking the transmembrane region, resulting in a soluble HMG CoA reductase enzyme) provides higher HMG CoA reductase activity and thus increased delta-5 steroid compound production over the same case with an introduced full-length HMG CoA reductase gene. A useful truncated HMG CoA reductase nucleic acid encodes at least the catalytic domain.

Hydroxymethylglutaryl-CoA reductase is enzyme number 1.1.1.88, using the recommended nomenclature of the International Union of Biochemistry and Molecular Biology on the Nomenclature and Classification of Enzymes, Enzyme Nomenclature 1992, Edwin C. Webb, ed., Academic Press, Inc. (San Diego, California: 1992), page 35.

The present invention contemplates transforming a plant cell with a structural gene that encodes a polypeptide having HMG-CoA reductase activity. The HMG-CoA reductase enzymes of both animal and yeast cells comprise three distinct amino acid residue sequence regions, which regions are designated the catalytic region, the membrane-binding region and the linker region.

The catalytic region contains the active site of the HMG-CoA reductase enzyme and comprises about forty percent of the COOH-terminal portion of intact HMG-CoA reductase enzyme.

5 The membrane-binding region contains hydrophobic amino acid residues and comprises about fifty percent of the NH₂-terminal portion of intact HMG-CoA reductase enzyme.

 The linker region connects the catalytic and membrane-binding regions, and constitutes the remaining about ten
10 percent of the intact enzyme.

 As discussed in greater detail below, only the catalytic region of HMG-CoA reductase is needed herein to provide the desired enzyme activity. Thus, an exogenous structural gene that encodes a polypeptide corresponding to
15 that catalytic region is the minimal HMG Co A reductase gene required for transforming plant cells in addition to one of the steroid pathway enzymes discussed below. The present invention therefore contemplates use of both intact and truncated structural genes that encode a polypeptide having
20 HMG-CoA reductase activity.

 A structural gene encoding a polypeptide having HMG-CoA reductase activity can be obtained or constructed from a variety of sources and by a variety of methodologies. See, e.g. Carlson et al., *Cell*, 28:145 (1982); Rine et al., *Proc.*
25 *Natl. Acad. Sci. USA*, 80:6750 (1983). Exemplary of such structural genes are the mammalian and yeast genes encoding HMG-CoA reductase or the catalytic region thereof.

 The disclosures of Chappell, et al., U.S. Patent No. 5,349,126, are incorporated in full herein by reference.
30 The mammalian genome contains a single gene encoding HMG-CoA reductase. The nucleotide sequence of the hamster and human gene for HMG-CoA reductase have been described in Chappell et al. A composite nucleotide sequence of DNA corresponds to the mRNA SEQ ID NO:1 of Chappell et al., as well as the

derived amino acid residue sequence SEQ ID NO:2 of Chappell et al., for hamster HMG-CoA reductase is provided in Fig. 2 of Chappell et al, reprinted from Chin et al., *Nature*, 308:613 (1984). The composite nucleotide sequence of Fig. 2, SEQ ID NO:1 of Chappell et al., comprising about 4768 base pairs, includes the nucleotide sequence encoding the intact hamster HMG-CoA reductase enzyme.

Intact hamster HMG-CoA reductase comprises about 887 amino acid residues (SEQ ID NO:2 of Chappell et al.). A structural gene encoding an intact hamster HMG-CoA reductase enzyme of 887 amino acid residues comprises base pairs from about nucleotide position 164 to about nucleotide position 2824 of SEQ ID NO:1 of Chappell et al.

A preferred structural gene is one that encodes a polypeptide corresponding to only the catalytic region of the enzyme. Two catalytically active segments of hamster HMG-CoA reductase have been defined. Liscum et al., *J. Biol. Chem.*, 260(1):522 (1985). One segment containing a catalytic region has an apparent molecular weight of 62 kDa and comprises amino acid residues from about position 373 to about position 887. A second segment containing a catalytic region has an apparent molecular weight of 53 kDa segment and comprises amino acid residues from about position 460 to about position 887. The 62 kDa catalytically active segment is encoded by base pairs from about nucleotide position 1280 to about nucleotide position 2824 of SEQ ID NO:1 of Chappell et al. The 53 kDa catalytically active segment is encoded by base pairs from about nucleotide position 1541 to about nucleotide position 2824 of SEQ ID NO:1 of Chappell et al.

In a preferred embodiment, the utilized structural gene encodes the catalytic region and at least a portion of the linker region of HMG-CoA reductase. The linker region of hamster HMG-CoA reductase comprises amino acid residues from about position 340 to about position 373 or from about

position 340 to about position 460, depending upon how the catalytic region is defined. These linker regions are encoded by base pairs from about nucleotide position 1180 to about nucleotide position 1283 or from about position 1180
5 to about position 1540, respectively of SEQ ID NO:1 of Chappell et al. The structural gene encoding the linker region is operatively linked to the structural gene encoding the catalytic region.

In one particularly preferred embodiment, a structural
10 gene encoding a catalytically active, truncated HMG-CoA reductase enzyme can optionally contain base pairs encoding a small portion of the membrane region of the enzyme.

A structural gene encoding a polypeptide comprising a catalytically active, truncated or intact HMG-CoA reductase
15 enzyme from other organisms such as yeast can also be used in accordance with the present invention.

Yeast cells contain two genes encoding HMG-CoA reductase. The two yeast genes, designated HMG1 and HMG2, encode two distinct forms of HMG-CoA reductase, designated
20 HMG-CoA reductase 1 SEQ ID NO:3 of Chappell et al. are presented in Fig. 3 of Chappell et al., are taken from Basson et al. *Mol. Cell Biol.*, 8(9):3797 (1988). The nucleotide base sequences of HMG2 SEQ ID NO:5 of Chappell et al. as well as the amino acid residue sequence of HMG-CoA
25 reductase 2 SEQ ID NO:6 of Chappell et al. are set forth therein in the Sequence Listing.

The entire HMG1 gene comprises about 3360 base pairs SEQ ID NO:3 of Chappell et al. Intact HMG-CoA reductase 1 comprises an amino acid sequence of about 1054 amino acid
30 residues SEQ ID NO:4 of Chappell et al. Thus, the minimal portion of the HMG1 gene that encodes an intact enzyme comprises base pairs from about nucleotide position 121 to about position 3282 of Fig. 3, SEQ ID NO:3 of Chappell et al.

The entire HMG2 gene comprises about 3348 base pairs SEQ ID NO:5 of Chappell et al. Intact HMG-CoA reductase 2 comprises about 1045 amino acid residues SEQ ID NO:6 of Chappell et al. Thus, the minimal portion of HMG2 gene that
5 encodes intact HMG-CoA reductase 2 comprises base pairs from about nucleotide position 121 to about position 3255 of SEQ ID NO:5 of Chappell et al.

By analogy to the truncated hamster structural gene, structural genes encoding polypeptides comprising
10 catalytically active, truncated HMG-CoA reductase enzymes from yeast can also be used in accordance with the present invention.

The catalytic region of HMG-CoA reductase 1 comprises amino acid residues from about residue 618 to about residue
15 1054: i.e., the COOH-terminus. A structural gene that encodes the catalytic region comprises base pairs from about nucleotide position 1974 to about position 3282 of Fig. 3 of Chappell et al.

The linker region of HMG-CoA reductase 1 comprises an amino acid sequence from about residue 525 to about residue
20 617. A structural gene that encodes the linker region comprises nucleotides from about position 1695 to about position 1973 of Fig. 3 of Chappell et al. A structural gene encoding the linker region of the enzyme operatively
25 linked to the structural gene encoding the catalytic region of the enzyme.

Also by analogy to the truncated hamster gene, a truncated HMG1 gene can optionally contain nucleotide base pair sequences encoding a small portion of the membrane-
30 binding region of the enzyme. Such a structural gene preferably comprises base pairs from about nucleotide position 121 to about position 147 and from about position 1695 to about position 3282 of Fig. 3 of Chappell et al.

A construct similar to those above from an analogous portion of yeast HMG-CoA reductase 2 can also be utilized.

A nucleic acid sequence encoding HMG-CoA reductase from *Hevea brasiliensis* has been disclosed by Chye et al. (1991) *Plant Mol. Biol.* 16: 567-577. A nucleic acid sequence encoding an *Arabidopsis thaliana* HMG-CoA reductase has been published by Caelles et al. (1989) *Plant Mol. Biol.* 13: 627-638, and is also available as GenBank accession number L19261. U.S. Patents Nos. 5,306,862 and 5,365,017 disclose additional DNA sequences encoding HMG-CoA reductases.

The following sequences are listed by Genbank Accession numbers:

026662 methanobacterium thermoautotrophicum. 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 12/1998

Q58116 methanococcus jannaschii. 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 7/1998

Q59468 halobacterium volcanii (haloferax volcanii). 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 7/1998

O08424 sulfolobus solfataricus. 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 12/1998

M22255 Saccharomyces cerevisiae Yeast HMG-CoA reductase (HGM2) gene, complete cds; 3-hydroxy-3-methyl glutaryl coenzyme A reductase. 4/1993

M22002 Saccharomyces cerevisiae Yeast HMG-CoA reductase (HGM1) gene, complete cds; 3-hydroxy-3-methyl-glutaryl coenzyme A reductase. 4/1993

Q12649 phycomyces blakesleeenanus. 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase) (fragment). 11/1997

Q12577 fusarium moniliforme (gibberella fujikuroi). 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg- coa reductase). 11/1997

AB012603 Candida utilis Candida utilis HMG mRNA for
5 HMG-CoA reductase, complete cds. 7/1998

P34136 dictyostelium discoideum (slime mold). 3-hydroxy-3-methylglutaryl-coenzyme a reductase 2 (ec 1.1.1.34) (hmg- coa reductase 2) (fragment).35735

PQ0761 hydroxymethylglutaryl-CoA reductase (NADPH) (EC
10 1.1.1.34) (HMGR 10) - wheat (fragment)

P48019 oryza sativa (rice). 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase) (fragment). 2/1996

O24594 zea mays (maize). 3-hydroxy-3-methylglutaryl
15 coenzyme a reductase (ec 1.1.1.88). 5/1999

PQ0763 hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) (HMGR 23) - wheat (fragment)

PQ0762 hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) (HMGR 18) - wheat (fragment)
20 from proprietary soy sequence database

Q00583 hevea brasiliensis (para rubber tree). 3-hydroxy-3-methylglutaryl-coenzyme a reductase 3 (ec 1.1.1.34) (hmg- coa reductase 3). 7/1998

Q03163 catharanthus roseus (rosy periwinkle)
25 (madagascar periwinkle). 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 7/1998

P48022 lycopersicon esculentum (tomato). 3-hydroxy-3-methylglutaryl-coenzyme a reductase 2 (ec 1.1.1.34) (hmg-coa reductase 2). 7/1998

30 Q01559 nicotiana glauca (wood tobacco). 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 7/1998

L01400 *Solanum tuberosum* Potato hydroxymethylglutaryl coenzyme A reductase (hmgr) mRNA, complete cds; putative. 4/1996

Q43826 *raphanus sativus* (radish).

- 5 hydroxymethylglutaryl-coa reductase (ec 1.1.1.34)
(hydroxymethylglutaryl-coa reductase (nadph)) (3-hydroxy-3-methylglutaryl-coenzyme a red

L19261 *Arabidopsis thaliana* *Arabidopsis thaliana* HMG-CoA reductase gene, complete cds. 4/1994

- 10 AB021862 *Cucumis melo* *Cucumis melo* mRNA for HMG-CoA reductase, complete cds; putative. 1/1999

P29058 *hevea brasiliensis* (para rubber tree). 3-hydroxy-3-methylglutaryl-coenzyme a reductase 2 (ec 1.1.1.34) (hmg- coa reductase 2) (fragment).35735

- 15 P29057 *hevea brasiliensis* (para rubber tree). 3-hydroxy-3-methylglutaryl-coenzyme a reductase 1 (ec 1.1.1.34) (hmg- coa reductase 1). 7/1998

- P48021 *camptotheca acuminata*. 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 11/1997

P43256 *arabidopsis thaliana* (mouse-ear cress). 3-hydroxy-3-methylglutaryl-coenzyme a reductase 2 (ec 1.1.1.34) (hmg- coa reductase 2) (hmgr2). 7/1998

- 25 P00347 *cricetulus griseus* (chinese hamster). 3-hydroxy-3-methylglutaryl-coenzyme A reductase (ec 1.1.1.34) (hmg-coA reductase). 11/1997

- L00183 *Cricetulus* sp. Hamster 3-hydroxy-3-methylglutaryl coenzyme A (HMG CoA) reductase gene, exons 19 and 20; 3-hydroxy-3-methylglutaryl coenzyme A (HMG CoA). 4/1993

M12705 *Mesocricetus auratus* Syrian hamster 3-hydroxy-3-methylglutaral coenzyme A reductase (HMG-CoA reductase) mRNA, complete cds; 3-hydroxy-3-methylglutaral coenzyme A red

P51639 *rattus norvegicus* (rat). 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 12/1998

Q29512 *oryctolagus cuniculus* (rabbit). 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 7/1999

M11058 *Homo sapiens* Human 3-hydroxy-3-methylglutaryl coenzyme A reductase mRNA, complete cds; 3-hydroxy-3-methylglutaryl coenzyme A reductase. 11/1994

10 M62766 *Mus musculus* Mouse HMG-CoA reductase mRNA, 3' end. 4/1993

P20715 *xenopus laevis* (african clawed frog). 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 11/1997

15 P16393 *strongylocentrotus purpuratus* (purple sea urchin). 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 11/1997

P54960 *blattella germanica* (german cockroach). 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 11/1997

P14773 *drosophila melanogaster* (fruit fly). 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 12/1998

25 P34135 *dictyostelium discoideum* (slime mold). 3-hydroxy-3-methylglutaryl-coenzyme a reductase 1 (ec 1.1.1.34) (hmg-coa reductase 1). 11/1997

P16237 *schistosoma mansoni* (blood fluke). 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 7/1998

30 O28538 *archaeoglobus fulgidus*. 3-hydroxy-3-methylglutaryl-coenzyme a reductase (ec 1.1.1.34) (hmg-coa reductase). 12/1998

M24015 *Pseudomonas mevalonii* P.mevalonii HMG-CoA reductase (mvaA) gene, complete cds; HMG-CoA reductase (EC 1.1.1.88). 4/1993

5 B. Steroid Pathway Enzymes

The present invention contemplates nucleic acid sequences encoding polypeptides having the enzyme activity of the steroid pathway enzymes squalene epoxidase, sterol methyl transferase I, sterol C4-demethylase, obtusifoliol C14 α -demethylase, sterol C5-desaturase and sterol methyl transferase II.

 i. Squalene Epoxidase

Squalene epoxidase (also called squalene monooxygenase) catalyzes the conversion of squalene to squalene epoxide (2,3-oxidosqualene), a precursor to the initial sterol molecule in phytosterol biosynthetic pathway, cycloartenol. This is the first reported step in the pathway where oxygen is required for activity. The formation of squalene epoxide is also the last common reported step in sterol biosynthesis of animals, fungi and plants. Recently, several homologues of *Arabidopsis* and *Brassica* squalene epoxidase genes were reported (Schafer, U.A., Reed, D.W., Hunter, D.G., Yao, K., Weninger, A.M., Tsang, E.W., Reaney, M.J., MacKenzie, S.L., and Covello, P.S. (1999). *Plant Mol. Biol.* 39(4): 721-728). The same authors also have a PCT application disclosing the use of antisense technology with squalene epoxidase to elevate squalene levels in plants (WO 97/34003). However, to date there are no reports on functional characterization of any plant squalene epoxidase gene or enzyme.

Squalene Epoxidase, also known as squalene monooxygenase is enzyme reference number 1.14.99.7, Enzyme Nomenclature 1992, p. 146.

Several squalene epoxidase enzymes are known to the art. These include *Arabidopsis* squalene epoxidase protein sequence Accession No. AC004786 (SEQ ID NO:1), *Arabidopsis* squalene epoxidase Accession No. N64916 (SEQ ID NO:2), and
5 *Arabidopsis* squalene epoxidase Accession No. T44667 (SEQ ID NO:3). Japanese patent application No. 07194381 A discloses a DNA encoding a mammalian squalene epoxidase.

In order to facilitate the modifications to sterol biosynthesis and accumulation described herein, the present
10 invention also provides an isolated DNA molecule, comprising a nucleotide sequence selected from the group consisting of:

(a) *Arabidopsis* squalene epoxidase from clone ID ATA506263 disclosure SEQ ID NO:4, clone ID ATA304243 disclosure SEQ ID NO:6, clone ID ATA102071 disclosure SEQ ID
15 NO: 8, clone ATA504158 disclosure SEQ ID NO:10, or the complement thereof;

(b) a nucleotide sequence that hybridizes to said nucleotide sequence of (a) under a wash stringency equivalent to 0.5X SSC to 2X SSC, 0.1% SDS, at 55-65°C, and
20 which encodes a polypeptide having squalene epoxidase enzymatic activity substantially similar to that of the disclosed squalene epoxidase;

(c) a nucleotide sequence encoding the same genetic information as said nucleotide sequence of (a), but which is
25 degenerate in accordance with the degeneracy of the genetic code; and

(d) a nucleotide sequence encoding the same genetic information as said nucleotide sequence of (b), but which is degenerate in accordance with the degeneracy of the genetic
30 code.

An additional aspect of the invention is the recombinant constructs and vectors (pMON48343, Fig. 30; pMON43844, Fig. 31) comprising nucleic acid sequences encoding the novel squalene epoxidase, as well as a method

of producing the novel squalene epoxidase, comprising culturing a host cell transformed with the novel constructs or vectors for a time and under conditions conducive to the production of the squalene epoxidase, and recovering the squalene epoxidase produced thereby.

ii. Sterol Methyl Transferase I

S-adenosyl-L-methionine:sterol C-24 methyl transferases (SMT1 and SMT2) catalyze the transfer of a methyl group from a cofactor, S-adenosyl-L-methionine, to the C-24 center of the sterol side chain (Bach, T.J. and Benveniste, P. (1997), Prog. Lipid Res. 36: 197-226). SMT in higher plant cells are responsible for their capability to produce a mixture of 24-methyl and 24-ethyl sterols (Schaffer, A., Bouvier-Navé, Benveniste, P., Schaller, H. (2000) Lipids 35: 263-269). Functional characterization of the SMT using a yeast *erg6* expression system demonstrated unambiguously that an SMT1 sequence encodes a cycloartenol-C24-methyltransferase and a SMT2 sequence encodes a 24-methylene lophenol-C24-methyltransferase in a given plant species (Bouvier-Navé, P., Husselstein, T., and Benveniste, P. (1998), Eur. J. Biochem. 246: 518-529). Several plant genes coding for SMT1 and SMT2 have been reported and reviewed (Schaffer, A., Bouvier-Navé, Benveniste, P., Schaller, H. (2000) Lipids 35: 263-269). Transgenic plants expressing homologues of either SMT1 or SMT2 have been studied (Schaffer, A., Bouvier-Navé, Benveniste, P., Schaller, H. (2000) Lipids 35: 263-269). The use of these genes to modify plant sterol composition are also covered by two Monsanto patent applications (WO 98/45457 and WO 00/61771).

Sterol methyl transferase I enzymes known in the art are useful in the present invention. Exemplary sequences include the known *Arabidopsis* sterol methyl transferase I protein sequence Accession No. U71400 (disclosure SEQ ID

NO:19), the known tobacco sterol methyl transferase I protein sequence Accession No. U81312 (disclosure SEQ ID NO:20) and *Ricinus communis* sterol-C-methyltransferase, *Eur. J. Biochem.*, 246(2), 518-529 (1997). (Complete cds, Accession No. g2246457).

S-Adenosyl-L-Methionine-Sterol-C24-Methyltransferase--A nucleic acid sequence encoding an *Arabidopsis thaliana* S-adenosyl-L-methionine-sterol-C24-methyltransferase has been published by Husselstein et al. (1996) *FEBS Letters* 381: 87-92. Δ^{24} -sterol C-methyltransferase is enzyme number 2.1.1.41, Enzyme Nomenclature 1992, page 160.

iii. Sterol C4-Demethylase

Sterol C-4 demethylase catalyses the first of several demethylation reactions, which results in the removal of the two methyl groups at C-4. While in animals and fungi the removal of the two C-4 methyl groups occurs consecutively, in plants it has been reported that there are other steps between the first and second C-4 demethylations (Bach, T.J. and Benveniste, P. (1997), *Prog. Lipid Res.* 36: 197-226). The C-4 demethylation is catalyzed by a complex of microsomal enzymes consisting of a monooxygenase, an NAD⁺-dependent sterol 4-decarboxylase and an NADPH-dependent 3-ketosteroid reductase.

iv. Obtusifoliol C14 α -Demethylase

Sterol C-14 demethylase catalyzes demethylation at C-14 which removes the methyl group at C-14 and creates a double bond at that position. In both fungi and animals, this is the first step in the sterol synthesis pathway. However, in higher plants, the 14 α -methyl is removed after one C-4 methyl has disappeared. Thus, while lanosterol is the

substrate for C-14 demethylase in animal and fungal cells, the plants enzyme uses obtusifoliol as substrate. Sterol 14-demethylation is mediated by a cytochrome P-450 complex. The mechanism of 14 α -methyl removal involves two oxidation steps leading to an alcohol, then an aldehyde at C-29 and a further oxidative step involving a deformylation leading to formic acid and the sterol product with a typical 8,14-diene (Aoyama, Y., Yoshida, Y., Sonoda, Y., and Sato, Y. (1989) J. Biol. Chem. 264: 18502-18505). Obtusifoliol 14 α -demethylase from *Sorghum bicolor* (L) Moench has been cloned using a gene-specific probe generated using PCR primers designed from an internal 14 amino acid sequence and was functionally expressed in *E. coli* (Bak, S, Kahn, R.A., Olsen, C.E. and Halkier, B.A. (1997) The Plant Journal 11(2): 191-201). Also, *Saccharomyces cerevisiae* CYP51A1 encoding lanosterol-14-demethylase was functionally expressed in tobacco (Grausem, B., Chaubet, N., Gigot, C., Loper, J.C., and Benveniste, P. (1995) The Plant Journal 7(5): 761-770).

Sterol C-14 demethylase enzymes and sequences are known in the art. For example *Sorghum bicolor* obtusifoliol 14 α -demethylase CYP51 mRNA, described in Plant J., 11(2):191-201 (1997) (complete cds Acession No. U74319). In order to facilitate the modifications to sterol biosynthesis and accumulation described herein, the present invention also provides an isolated DNA molecule, having a nucleotide sequence selected from the group consisting of:

(a) obtusifoliol C14 α -demethylase from clone ID: ATA101105 disclosure SEQ ID NO:14, clone ID ATA202967 disclosure SEQ ID NO:15, clone ID ATA403931 disclosure SEQ ID NO:17, or the complement thereof;

(b) a nucleotide sequence that hybridizes to said nucleotide sequence of (a) under a wash stringency equivalent to 0.5X SSC to 2X SSC, 0.1% SDS, at 55-65°C, and

which encodes a polypeptide having obtusifoliol C14 α -demethylase enzymatic activity substantially similar to that of the disclosed obtusifoliol C14 α -demethylase;

(c) a nucleotide sequence encoding the same genetic information as said nucleotide sequence of (a), but which is degenerate in accordance with the degeneracy of the genetic code; and

(d) a nucleotide sequence encoding the same genetic information as said nucleotide sequence of (b), but which is degenerate in accordance with the degeneracy of the genetic code.

An additional aspect of the invention is the recombinant constructs and vectors (pMON43842, Fig.29) comprising nucleic acid sequences encoding the novel obtusifoliol C14 α -demethylase, as well as a method of producing the novel obtusifoliol C14 α -demethylase, comprising culturing a host cell transformed with the novel constructs or vectors for a time and under conditions conducive to the production of the obtusifoliol C14 α -demethylase, and recovering the obtusifoliol C14 α -demethylase produced thereby.

v. Sterol C5-Desaturase

Sterol C-5 desaturase catalyzes the insertion of the Δ^5 -double bond that normally occurs at the Δ^7 -sterol level, thereby forming a $\Delta^{5,7}$ -sterol (Parks et al., *Lipids* 30:227-230 (1995)). The reaction has been reported to involve the stereospecific removal of the 5 α and 6 α hydrogen atoms, biosynthetically derived from the 4 pro-R and 5 pro-S hydrogens of the (+) and (-) R-mevalonic acid, respectively (Goodwin, T.W. (1979) *Annu. Rev. Plant Physiol.* 30: 369-404). The reaction is obligatorily aerobic and requires NADPH or NADH. The desaturase has been reported to be a

multienzyme complex present in microsomes. It consists of the desaturase itself, cytochrome b₅ and a pyridine nucleotide-dependent flavoprotein. The Δ^5 -desaturase is reported to be a mono-oxygenase that utilizes electrons derived from a reduced pyridine nucleotide via cytochrome_b (Taton, M., and Rahier, A. (1996) Arch. Biochem. Biophys. 325: 279-288). An *Arabidopsis thaliana* cDNA encoding a sterol-C5-desaturase was cloned by functional complementation of a yeast mutant, *erg3* defective in *ERG3*, the gene encoding the sterol C5-desaturase required for ergosterol biosynthesis (Gachotte D., Husselstein, T., Bard, M., Lacroute F., and Benveniste, P. (1996) The Plant Journal 9(3): 391-398). Known sterol C5-desaturase enzymes are useful in the present invention, including *Arabidopsis* sterol C5-desaturase protein sequence Accession No. X90454, disclosure SEQ ID NO:22, and the *Arabidopsis thaliana* mRNA for sterol-C5-desaturase described in *Plant J.* 9(3):391-398 (1996) (complete cds Accession No. g1061037).

The NCBI (National Center for Biotechnology Information) database shows 37 sequences for sterol desaturase that are useful in the present invention. The following are exemplary of such sequences. From yeast: C5 sterol desaturase NP_013157 (*Saccharomyces cerevisiae*); hypothetical C5 sterol desaturase-fission T40027 (*Schizosaccharomyces pombe*); C5 sterol desaturase-fission T37759 (*Schizosaccharomyces pombe*); C5 sterol desaturase JQ1146 (*Saccharomyces cerevisiae*); C5 sterol desaturase BAA21457 (*Schizosaccharomyces pombe*); C5 sterol desaturase CAA22610 (*Schizosaccharomyces pombe*); putative C5 sterol desaturase CAA16898 (*Schizosaccharomyces pombe*); probable C5 sterol desaturase O13666 (*erg3_schpo*); C5 sterol desaturase P50860 (*Erg3_canga*); C5 sterol desaturase P32353 (*erg3_yeast*); C5,6 desaturase AAC99343 (*Candida albicans*); C5 sterol desaturase BAA20292 (*Saccharomyces cerevisiae*); C5

sterol desaturase AAB39844 (*Saccharomyces cerevisiae*); C5
sterol desaturase AAB29844 (*Saccharomyces cerevisiae*); C5
sterol desaturase CAA64303 (*Saccharomyces cerevisiae*); C5
sterol desaturase AAA34595 (*Saccharomyces cerevisiae*); C5
5 sterol desaturase AAA34594 (*Saccharomyces cerevisiae*). From
plants: C5 sterol desaturase S71251 (*Arabidopsis thaliana*);
putative sterol-C5-desaturase AAF32466 (*Arabidopsis*
thaliana); sterol-C5-desaturase AAF32465 (*Arabidopsis*
thaliana); putative sterol desaturase AAF22921 (*Arabidopsis*
10 *thaliana*); delta7 sterol C5 desaturase (*Arabidopsis*
thaliana); sterol C5(6) desaturase homolog AAD20458
(*Nicotiana tabacum*); sterol C5 desaturase AAD12944
(*Arabidopsis thaliana*); sterol C5,6 desaturase AAD04034
(*Nicotiana tabacum*); sterol C5 desaturase CAA62079
15 (*Arabidopsis thaliana*). From mammals: sterol-C5-desaturase
(*Mus musculus*) BAA33730; sterol-C5-desaturase BAA33729 (*Homo*
sapiens); lathosterol oxidase CAB65928 (*Leishmania major*);
lathosterol oxidase (lathosterol 5-desaturase) O88822 (*Mus*
musculus); lathosterol 5-desaturase O75845 (*Homo sapiens*);
20 delta7 sterol C5 desaturase AAF00544 (*Homo sapiens*).
Others: fungal sterol C5 desaturase homolog BAA18970 (*Homo*
sapiens).

For DNA sequences encoding a sterol-C5-desaturase
useful in the present invention, the NCBI_nucleotide search
25 for "sterol desaturase" came up with 110 sequences. The
following are exemplary of such sequences. NC_001139
(*Saccharomyces cerevisiae*); NC_001145 (*Saccharomyces*
cerevisiae); NC_001144 (*Saccharomyces cerevisiae*); AW700015
(*Physcomitrella patens*); AB004539 (*Schizosaccharomyces*
pombe); and AW596303 (*Glycine max*); AC012188 (*Arabidopsis*
30 *thaliana*).

vi. Sterol Methyl Transferase II

The combination of introduction of an HMG-CoA reductase gene along with a sterol methyl transferase II gene into a cell serves to reduce steroid pathway intermediate compound accumulation in addition to reducing the accumulation of 24-methyl sterols such as campesterol.

Known sterol methyl transferase II enzymes are useful in the present invention, including *Arabidopsis* sterol methyl transferase II protein sequence (complete mRNA cds from *FEBS Lett.* 381(12):87-92 (1996) Accession No. X89867), disclosure SEQ ID NO:21.

Recombinant constructs encoding any of the forgoing enzymes affecting the steroid biosynthetic pathway can be incorporated into recombinant vectors comprising the recombinant constructs comprising the isolated DNA molecules. Such vectors can be bacterial or plant expression vectors.

IV. Recombinant Constructs and Vectors

The present invention contemplates a recombinant construct that contains a DNA sequence encoding a polypeptide exhibiting 3-hydroxy-3-methylglutaryl-Coenzyme A (HMG-CoA) reductase activity and a DNA sequence encoding a polypeptide exhibiting the activity of a steroid pathway enzyme. Each polypeptide-encoding DNA sequence is operably linked in the 5' to 3' direction independent of the other sequence. Each DNA sequence in the 5' to 3' direction comprises a promoter, then the DNA sequence encoding the polypeptide then a transcription termination signal sequence. The steroid pathway enzyme is a squalene epoxidase enzyme, a sterol methyl transferase I enzyme, a sterol C4-demethylase enzyme, a obtusifolius C14 α -demethylase enzyme, a sterol C5-desaturase enzyme, or a sterol methyl transferase II enzyme.

Preferably, the promoters in the recombinant construct are seed-specific promoters. In one embodiment, the promoter is derived from a species in a different order from the host cell. In other embodiments, the encoded HMG CoA reductase and/or steroid pathway enzymes is(are) from a species in a different order from the order that of the host cell.

It is contemplated that a construct comprises more than one of the DNA sequences encoding a steroid pathway enzyme.

The invention also contemplates a recombinant vector comprising the above-described recombinant construct, wherein that vector is preferably a plant expression vector.

A recombinant DNA molecule of the present invention can be produced by operatively linking a vector to a useful DNA segment discussed herein to form a plasmid. A vector capable of directing the expression of a polypeptide having HMG-CoA reductase activity is referred to herein as an HMG-CoA reductase "plant integrating vector".

Such plant integrating vectors contain control elements that direct and regulate expression, including a promoter, a marker, a terminator and insertion sequence (e.g. FIG. 5). The polypeptide coding genes are operatively linked to the plant integrating vector to allow the promoter sequence to direct RNA polymerase binding and expression of the desired polypeptide coding gene.

Useful in expressing the polypeptide coding gene are promoters that are inducible, viral, synthetic, constitutive as described by Poszkowski et al., *EMBO J.*, 3:2719 (1989) and Odell et al., *Nature*, 313:810 (1985), and temporally regulated, spatially regulated and spatiotemporally regulated as given in Chau et al., *Science*, 244:174-181 (1989). The promoter preferably comprises a promoter sequence whose function in regulating expression of the structural gene is substantially unaffected by the amount of

sterol or squalene in the cell. As used herein, the term "substantially unaffected" means that the promoter is not responsive to direct feedback control by the sterols or squalene accumulated in transformed cells or transgenic plants.

A promoter is also selected for its ability to direct the transformed plant cell's or transgenic plant's transcriptional activity to the structural gene encoding a polypeptide having HMG-CoA reductase activity. Structural genes can be driven by a variety of promoters in plant tissues. Promoters can be near-constitutive, such as the CaMV 35S promoter, or tissue specific or developmentally specific promoters affecting dicots or monocots.

As exemplified and discussed in detail herein, where the near-constitutive promoter CaMV 35S is used to transform tobacco plants, increases in total sterol and squalene accumulation are found in a variety of transformed plant tissues (e.g. callus, leaf, seed and root). Alternatively, the effects of transformation (e.g. increased amount of a gene coding for HMG-CoA reductase, increased total sterol accumulation and increased squalene accumulation) can be directed to specific plant tissues by using plant integrating vectors containing a tissue-specific promoter.

An exemplary tissue-specific promoter is the Lectin promoter, which is specific for seed tissue. The Lectin protein in soybean seeds is encoded by a single gene (Lel) that is only expressed during seed maturation and accounts for about 2 to about 5 percent of total seed mRNA. The Lectin gene and seed-specific promoter have been fully characterized and used to direct seed specific expression in transgenic tobacco plants. See, e.g., Vodkin et al., *Cell*, 34:1023 (1983) and Lindstrom et al., *Developmental Genetics*, 11:160 (1990).

A plant integrating vector containing a structural gene coding for a polypeptide having HMG-CoA reductase activity is engineered to be under control of the Lectin promoter and that vector is introduced into soybean plants using a protoplast transformation method. E.G. Dhir et al., *Plant Cell Reports*, 10:97 (1991). The expression of the polypeptide having HMG-CoA reductase activity is directed specifically to the seeds of the transgenic plant. In this way, a transgenic soybean seed having increased squalene accumulation is produced. Such seeds can then be used to extract oil containing enhanced levels of squalene. As set forth hereinafter, such squalene-enhanced oil is characterized by a greater thermal stability when compared to non-squalene-enhanced oil.

In the present invention, a plant has an exogenously provided structural gene for HMG-CoA reductase and at least one of the six enumerated steroid pathway enzymes, a squalene epoxidase enzyme, a sterol methyl transferase I enzyme, a sterol C4-demethylase enzyme, a obtusifoliol C14 α -demethylase enzyme, a sterol C5-desaturase enzyme, or a sterol methyl transferase II enzyme. The plant or seed thus containing these added genes is contemplated, while the methods to arrive at a plant or seed according to the invention are open to the multitude of methods contemplated by a person of ordinary skill in the art. In particular, all of the added structural genes do not have to have been added at the same time, or by the same route. Thus, for example, the HMG-CoA reductase activity may result from a cross with a plant made according to a process of U.S. Patent No. 5,349,126, while a steroid pathway enzyme is added by nucleic acid bombardment to that plant. Further, when more than one nucleotide sequence encoding a steroid pathway enzyme is present in a contemplated plant, the

expression of the gene does not have to be under the control of the same promoter, or even the same type of promoter.

The choice of which plant integrating vector and ultimately to which promoter a polypeptide coding gene is
5 operatively linked depends directly on the functional properties desired, e.g. the location and timing of protein expression, and the host cell to be transformed. These are well known limitations inherent in the art of constructing recombinant DNA molecules. However, a vector useful in
10 practicing the present invention is capable of directing the expression of the polypeptide coding gene, i.e., the gene encoding HMG-CoA reductase activity, included in the DNA segment to which it is operatively linked.

Typical vectors useful for expression of genes in
15 higher plants are well known in the art and include vectors derived from the tumor-inducing (Ti) plasmid of *Agrobacterium tumefaciens*, described by Rogers et al., *Meth. Enzymol.*, 153:253-277 (1987). However, several other plant integrating vector systems are known to function in plants
20 including pCamVCN transfer control vector described by Fromm et al. *Proc. Nat. Acad. Sci. USA*, 82:5824 (1985). Plasmid pCamVCN (available from Pharmacia, Piscataway, N.J.) includes the cauliflower mosaic virus CaMV 35S promoter.

The use of retroviral plant integrating vectors to form
25 the recombinant DNAs of the present invention is also contemplated. As used herein, the term "retroviral plant integrating vector" refers to a DNA molecule that includes a promoter sequence derived from the long terminal repeat (LTR) region of a retrovirus genome.

30 In preferred embodiments, the vector used to express the polypeptide coding gene includes a selection marker that is effective in a plant cell, preferably a drug resistance selection marker. One preferred drug resistance marker is the gene whose expression results in kanamycin resistance;

i.e., the chimeric gene containing the nopaline synthase promoter, Tn5 neomycin phosphotransferase II and nopaline synthase 3' nontranslated region described by Rogers et al., in *Methods for Plant Molecular Biology*, A. Weissbach and H. Weissbach eds., Academic Press Inc., San Diego, Calif. (1988).

A variety of methods have been developed to operatively link DNA to vectors via complementary cohesive termini or blunt ends. For instance, complementary homopolymer tracts can be added to the DNA segment to be inserted and to the vector DNA. The vector and DNA segment are then joined by hydrogen bonding between the complementary homopolymeric tails to form recombinant DNA molecules.

Alternatively, synthetic linkers containing one or more restriction endonuclease sites can be used to join the DNA segment to the plant integrating vector. The synthetic linkers are attached to blunt-ended DNA segments by incubating the blunt-ended DNA segments with a large excess of synthetic linker molecules in the presence of an enzyme that is able to catalyze the ligation of blunt-ended DNA molecules, such as bacteriophage T4 DNA ligase. Thus, the products of the reaction are DNA segments carrying synthetic linker sequences at their ends. These DNA segments are then cleaved with the appropriate restriction endonuclease and ligated into a plant integrating vector that has been cleaved with an enzyme that produces termini compatible with those of the synthetic linker. Synthetic linkers containing a variety of restriction endonuclease sites are commercially available from a number of sources including New England BioLabs, Beverly, Mass.

Also contemplated by the present invention are RNA equivalents of the above-described recombinant DNA molecules.

A preferred recombinant DNA molecules utilized in accordance with the present invention are pMON53733-pMON53740 (Figures 13-20).

5 A. Promoters and Target Tissues

Promoters useful in the present invention include those that confer appropriate cellular and temporal specificity of expression. Such promoters include those that are constitutive or inducible, environmentally- or
10 developmentally-regulated, or organelle-, cell-, or tissue-specific. Preferred promoters for use with the present invention promote expression of the introduced enzymes in the seed in the cytosol, although expression in plasmids or organelles of the seeds is also contemplated.

15 Often-used constitutive promoters include the CaMV 35S promoter (Odell et al. (1985) *Nature* 313: 810), the enhanced CaMV 35S promoter, the Figwort Mosaic Virus (FMV) promoter (Richins et al. (1987) *NAR* 20: 8451), the mannopine synthase (*mas*) promoter, the nopaline synthase (*nos*) promoter, and
20 the octopine synthase (*ocs*) promoter.

Useful inducible promoters include heat-shock promoters (Ou-Lee et al. (1986) *Proc. Natl. Acad. Sci. USA* 83: 6815; Ainley et al. (1990) *Plant Mol. Biol.* 14: 949), a nitrate-inducible promoter derived from the spinach nitrite
25 reductase gene (Back et al. (1991) *Plant Mol. Biol.* 17: 9), hormone-inducible promoters (Yamaguchi-Shinozaki et al. (1990) *Plant Mol. Biol.* 15: 905; Kares et al. (1990) *Plant Mol. Biol.* 15: 905), and light-inducible promoters associated with the small subunit of RuBP carboxylase and
30 LHCP gene families (Kuhlemeier et al. (1989) *Plant Cell* 1: 471; Feinbaum et al. (1991) *Mol. Gen. Genet.* 226: 449; Weisshaar et al. (1991) *EMBO J.* 10: 1777; Lam and Chua (1990) *Science* 248: 471; Castresana et al. (1988) *EMBO J.* 7: 1929; Schulze-Lefert et al. (1989) *EMBO J.* 8: 651).

Examples of useful tissue-specific, developmentally-regulated promoters include fruit-specific promoters such as the E4 promoter (Cordes et al. (1989) *Plant Cell* 1:1025), the E8 promoter (Deikman et al. (1988) *EMBO J.* 7: 3315), the
5 kiwifruit actinidin promoter (Lin et al. (1993) *PNAS* 90: 5939), the 2A11 promoter (Houck et al., U.S. Patent 4,943,674), and the tomato pZ130 promoter (U.S. Patents 5,175, 095 and 5,530,185); the β -conglycinin 7S promoter (Doyle et al. (1986) *J. Biol. Chem.* 261: 9228; Slighton and
10 Beachy (1987) *Planta* 172: 356), and seed-specific promoters (Knutzon et al. (1992) *Proc. Natl. Acad. Sci. USA* 89: 2624; Bustos et al. (1991) *EMBO J.* 10: 1469; Lam and Chua (1991) *J. Biol. Chem.* 266: 17131; Stayton et al. (1991) *Aust. J. Plant. Physiol.* 18: 507). Fruit-specific gene regulation is
15 discussed in U.S. Patent 5,753,475. Other useful seed-specific promoters include, but are not limited to, the napin, phaseolin, zein, soybean trypsin inhibitor, 7S, ADR12, ACP, stearoyl-ACP desaturase, oleosin, *Lasquerella* hydroxylase, and barley aldose reductase promoters (Bartels
20 (1995) *Plant J.* 7: 809-822), the EA9 promoter (U.S. Patent 5,420,034), and the Bce4 promoter (U.S. Patent 5,530,194). Useful embryo-specific promoters include the corn globulin 1 and oleosin promoters. Useful endosperm-specific promoters include the rice glutelin-1 promoter, the promoters for the
25 low-pI α -amylase gene (Amy32b) (Rogers et al. (1984) *J. Biol. Chem.* 259: 12234), the high-pI α -amylase gene (Amy 64) (Khurseed et al. (1988) *J. Biol. Chem.* 263: 18953), and the promoter for a barley thiol protease gene ("Aleurain") (Whittier et al. (1987) *Nucleic Acids Res.* 15: 2515).

30 Appropriate target tissues of plants for enhanced production of sterol compounds such as sitosterol, sitosterol esters, sitostanol, sitostanol esters, and tocopherols, and reduced production of campesterol, campestanol, and esters thereof, include, but are not

limited to, fruits, flowers, seeds, roots, tubers, leaves, stems, buds, and other vegetable parts of plants. Within seeds, appropriate organ compartments include the embryo, the endosperm, and the aleurone layer. Within any of the
5 noted target tissues, appropriate cellular compartments include, but are not limited to, the cell cytoplasm and plastids (e.g., proplastids, chloroplasts, chromoplasts, leucoplasts, amyloplasts, etc.).

10 B. Vectors

In plants, transformation vectors capable of introducing encoding DNAs involved in sterol compound and tocopherol biosynthesis are easily designed, and generally contain one or more DNA coding sequences of interest under
15 the transcriptional control of 5' and 3' regulatory sequences. Such vectors generally comprise, operatively linked in sequence in the 5' to 3' direction, a promoter sequence that directs the transcription of a downstream heterologous structural DNA in a plant; optionally, a 5'
20 non-translated leader sequence; a nucleotide sequence that encodes a protein of interest; and a 3' non-translated region that encodes a polyadenylation signal which functions in plant cells to cause the termination of transcription and the addition of polyadenylate nucleotides to the 3' end of
25 the mRNA encoding the protein. Plant transformation vectors also generally contain a selectable marker. Typical 5'-3' regulatory sequences include a transcription initiation start site, a ribosome binding site, an RNA processing signal, a transcription termination site, and/or a
30 polyadenylation signal. Vectors for plant transformation have been reviewed in Rodriguez et al. (1988) *Vectors: A Survey of Molecular Cloning Vectors and Their Uses*, Butterworths, Boston; Glick et al. (1993) *Methods in Plant Molecular Biology and Biotechnology* CRC Press, Boca Raton,

Fla; and Croy (1993) In *Plant Molecular Biology Labfax*, Hames and Rickwood, Eds., BIOS Scientific Publishers Limited, Oxford, UK.

5 The use of transit peptides, e.g. translational fusion peptides, are not preferred for use in conjunction with the enzymes of the present invention, where the sterol synthethic compounds are present primarily in the cellular cytosol.

10 V. Cell Transformation and Plant Regeneration

The amount of a gene coding for a polypeptide having HMG-CoA reductase activity is increased by transforming a desired plant cell with a suitable vector that contains that added exogenous structural gene. Expression of that gene in
15 the transformed plant cell and transgenic plants developed from that transformed plant cell enhances the activity of HMG-CoA reductase..

Methods for transforming polypeptide-coding genes into plant cells include *Agrobacterium*-mediated plant
20 transformation, protoplast transformation, gene transfer into pollen, injection into reproductive organs and injection into immature embryos. Each of these methods has distinct advantages and disadvantages. Thus, one particular methods of introducing genes into a particular plant strain
25 may not necessarily be the most effective for another plant strain, but it is well known which methods are useful for a particular plant strain.

Agrobacterium-mediated transfer is a widely applicable system for introducing genes into plant cells because the
30 DNA can be introduced into whole plant tissues, thereby bypassing the need for regeneration of an intact plant from a protoplast. The use of *Agrobacterium*-mediated plant integrating vectors to introduce DNA into plant cells is well known in the art. See, for example, the methods

described by Fraley et al., *Biotechnology*, 3:629 (1984) and Rogers et al., *Methods in Enzymology*, 153:253-277 (1987). Further the integration of the T8-DNA is a relatively precise process resulting in few rearrangements. The region
5 of DNA to be transferred is defined by the border sequences, and intervening DNA is usually inserted into the plant genome as described by Spielmann et al., *Mol. Gen. Genet.*, 205:34 (1986) and Jorgensen et al, *Mol. Gen. Genet.*, 207:471 (1987).

10 Modern *Agrobacterium* transformation vectors are capable of replication in *E. coli* as well as *Agrobacterium*, allowing for convenient manipulations as described by Klee et al., in *Plant DNA Infectious Agents*, T. Hohn and J. Schell, eds., Springer-Verlag, New York (1985) pp. 179-203.

15 Moreover, recent technological advances in vectors for *Agrobacterium*-mediated gene transfer have improved the arrangement of genes and restriction sites in the vectors to facilitate construction of vectors capable of expressing various polypeptide coding genes. The vectors described by
20 Rogers et al., *Meth. Enzymol.*, 153:253 (1987), have convenient multi-linker regions flanked by a promoter and a polyadenylation site for directed expression inserted polypeptide conding genes and are suitable for present purposes.

25 In addition, *Agrobacteria* containing both armed and disarmed Ti genes can be used for the transformations. Both types of transforming systems are illustrated herein. Transformants from the former system result in callus from which the desired squalene or sterol can be obtained,
30 whereas transformants obtained from the latter, disarmed Ti genes can be regenerated into complete transgenic plants from whose tissues, e.g. leaf, seed and root, the desired chemicals can be obtained.

In those plant strains where *Agrobacterium*-mediated transformation is efficient, it is the method of choice because of the facile and defined nature of the gene transfer.

5 *Agrobacterium*-mediated transformation of leaf disks and other tissues, such as cotyledons and hypocotyls, appears to be limited to plant strains that *Agrobacterium* naturally infects. *Agrobacterium*-mediated transformation is the most efficient in dicotyledonous plants. Few monocots appear to
10 be natural hosts for *Agrobacterium*, although transgenic plants have been produced in the monocot, asparagus, using *Agrobacterium* vectors as described by Bytebier et al., *Proc. Natl. Acad. Sci. USA*, 84:5345 (1987). Therefore, commercially important cereal grains such as rice, corn, and
15 wheat must usually be transformed using alternative methods. However, as mentioned above, the transformation of asparagus using *Agrobacterium* can also be achieved.

A transgenic plant formed using *Agrobacterium* transformation methods typically contains a single gene on
20 one chromosome. Such transgenic plants can be referred to as being heterozygous for the added gene. However, inasmuch as use of the word "heterozygous" usually implies the presence of a complementary gene at the same locus of the second chromosome of a pair of chromosomes, and there is no
25 such gene in a plant containing one more than one added gene as here, it is believed that a more accurate name for such a plant is an independent segregant, because the added, exogenous gene segregates independently during mitosis and meiosis. A transgenic plant containing a single structural
30 gene that encodes a polypeptide having HMG-CoA reductase activity and at least one of the enumerated 6 steroid pathway enzymes; i.e., and independent segregant, is a preferred transgenic plant.

More preferred is a transgenic plant that is homozygous for the added structural gene; i.e., a transgenic plant that contains two added genes, one gene at the same locus on each chromosome of a chromosome pair. A homozygous transgenic
5 plant can be obtained by sexually mating (selfing) an independent segregant transgenic plant that contains the added genes according to the invention, germinating some of the seed produced and analyzing the resulting plants produced for enhanced HMG-CoA reductase activity, steroid
10 pathway product accumulation or both, relative to a control (native, non-transgenic) or an independent segregant transgenic plant.

A homozygous transgenic plant exhibits enhanced HMG-CoA reductase activity as compared to a native, non-transgenic
15 plant and an independent segregant transgenic plant.

It is to be understood that two different transgenic plants can also be mated to produce offspring that contain two independently segregating added, exogenous genes. Selfing of appropriate progeny can produce plants that are
20 homozygous for both added, exogenous genes that encode a polypeptide having HMG-CoA reductase activity. Back-crossing to a parental plant and outcrossing with a non-transgenic plant are also contemplated.

25 A. Host Cells and Transformed Plant Cells

Cells modified according to the present invention are contemplated at each stage of the processes of the invention. As a result of the invention comprising at least two genes, there are several means to accomplish that end.
30 In some embodiments of the invention, the intermediate steps include transformation of nucleic acids comprising some or all of the genes into host cells.

The nucleic acid sequence encoding a polypeptide exhibiting HMGR activity does not have to be in the same

orientation as a nucleic acid sequence encoding a polypeptide exhibiting the activity of a steroid pathway enzyme. The coding nucleic acids can be under the control of different promoters or be in different orientations. For
5 the host plant cell useful in carrying out the steroid compound biosynthesis according to the invention, the minimum that is required is the coding nucleic acids be in the same host cell. As long as the HMGR and a steroid pathway enzyme coding sequences are present in the same host
10 cell, they do not have to be on the same DNA molecule or under the control of the same promoter, nor do they have to be derived from the same vector or construct.

Host cells are useful for making, storing, reproducing or manipulating nucleic acid constructs of the invention.
15 Contemplated host cells are eukaryotic cells, such as yeast or plant cells. Any plant cells can be utilized with the present invention. Some particularly useful agriculturally significant plant cells are canola, soybean, corn, maize, tobacco, cotton, rape, tomato and alfalfa. Other common
20 plant varieties are carrot, barley, arabidopsis, guayule and petunia. Prokaryotic host cells containing constructs and/or vectors according to the invention are also contemplated (e.g. *E. coli*).

One embodiment of the invention is a transformed host
25 cell containing inter alia a recombinant construct that encodes both a DNA sequence encoding a polypeptide exhibiting 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity and a DNA sequence encoding a steroid pathway enzyme, where the steroid pathway enzyme is as
30 described in detail above. In a preferred embodiment, those coding DNA sequences are operably linked to a promoter and a transcription termination signal sequence. In the coding sense direction of the construct, the components of the construct are operably linked in the 5' to 3' direction as a

promoter, the DNA sequence encoding sequence and a transcription termination signal sequence.

Another embodiment of the invention is host cell that has been transformed with a recombinant vector that has such
5 a construct. As discussed herein, in one embodiment of the invention, such a recombinant vector is a plant expression vector. Preferably such a host cell is a plant cell.

Methods of culturing various eukaryotic and prokaryotic cell cultures are well known in the art. The present
10 invention contemplates cell cultures of transformed host cells. Transformed plant cells include transformed protoplasts and other types of host cell intermediates as well as plant cell cultures.

Non-limiting examples of plants that can be used in the
15 practice of the invention include, acacia, alfalfa, aneth, apple, apricot, artichoke, arugula, asparagus, avocado, banana, barley, beans, beet, blackberry, blueberry, broccoli, brussel sprouts, cabbage, canola, cantaloupe, carrot, cassava, cauliflower, celery, cherry, chicory,
20 cilantro, citrus, clementines, coffee, corn, cotton, cucumber, Douglas fir, eggplant, endive, escarole, eucalyptus, fennel, figs, garlic, gourd, grape, grapefruit, honey dew, jicama, kiwifruit, lettuce, leeks, lemon, lime, Loblolly pine, mango, melon, mushroom, nectarine, nut, oat,
25 oil palm, oil seed rape, okra, onion, orange, ornamental plants, papaya, parsley, pea, peach, peanut, pear, pepper, persimmon, pine, pineapple, plantain, plum, pomegranate, poplar, potato, pumpkin, quince, radiata pine, radicchio, radish, raspberry, rice, rye, sorghum, Southern pine,
30 soybean, spinach, squash, strawberry, sugarbeet, sugarcane, sunflower, sweet potato, sweetgum, tangerine, tea, tobacco, tomato, triticale, turf, turnip, watermelon, wheat, yam, and zucchini.

Plants particularly attractive for the steroid pathway modifications described herein include those that produce carbon substrates which can be employed for synthesis of these compounds. Non-limiting examples of such plants include various monocots and dicots, including high oil seed plants such as high oil seed *Brassica* (e.g., *Brassica nigra*, *Brassica napus*, *Brassica hirta*, *Brassica rapa*, *Brassica campestris*, *Brassica carinata*, and *Brassica juncea*), soybean (*Glycine max*), castor bean (*Ricinus communis*), cotton, safflower (*Carthamus tinctorius*), sunflower (*Helianthus annuus*), flax (*Linum usitatissimum*), corn (*Zea mays*), coconut (*Cocos nucifera*), palm (*Elaeis guineensis*), oilnut trees such as olive (*Olea europaea*), sesame, and peanut (*Arachis hypogaea*), as well as *Arabidopsis*, tobacco, wheat, barley, oats, amaranth, potato, rice, tomato, and legumes (e.g., peas, beans, lentils, alfalfa, etc.).

Enhancement of sitostanol compound production by the methods discussed herein is expected to result in yields of sitostanol, sitostanol esters, or mixtures thereof in an amount of at least about 57% by weight, preferably from about 57% to about 90% by weight, and more preferably from about 57% to about 65% by weight of the total sterol compounds present in seed oil. Expressed on a seed dry weight basis, sitostanol, sitostanol esters, or mixtures thereof are expected to be present in an amount of at least about 0.08%, preferably from about 0.08% to about 0.8%, and more preferably from about 0.08% to about 0.4% of seed dry weight.

B. Processes of Transformation

A variety of different methods can be employed to introduce transformation/expression vectors into plant protoplasts, cells, callus tissue, leaf discs, meristems, etc., to generate transgenic plants. These methods include, for example, *Agrobacterium*-mediated transformation, particle

gun delivery, microinjection, electroporation, polyethylene glycol-mediated protoplast transformation, liposome-mediated transformation, etc. (reviewed in Potrykus (1991) *Ann. Rev. Plant Physiol. Plant Mol. Biol.* 42: 205).

5 In general, transgenic plants comprising cells containing and expressing nucleic acids encoding enzymes facilitating the modifications in sterol compound and tocopherol biosynthesis and accumulation described herein can be produced by transforming plant cells with a DNA
10 construct as described above via any of the foregoing methods; selecting plant cells that have been transformed on a selective medium; regenerating plant cells that have been transformed to produce differentiated plants; and selecting a transformed plant that expresses the enzyme-encoding
15 nucleotide sequence(s) at a level such that the amount of sitosterol, sitosterol esters, sitostanol, sitostanol esters, tocopherol compound(s), and campesterol/campestanol and their esters is within the ranges described herein.

 The encoding DNAs can be introduced either in a single
20 transformation event (all necessary DNAs present on the same vector), a co-transformation event (all necessary DNAs present on separate vectors that are introduced into plants or plant cells simultaneously), or by independent transformation events (all necessary DNAs present on
25 separate vectors that are introduced into plants or plant cells independently). Traditional breeding methods can subsequently be used to incorporate the desired combination of enzymes into a single plant, and to produce hybrid progeny of the invention plants.

30 Specific methods for transforming a wide variety of dicots and obtaining transgenic plants are well documented in the literature (Gasser and Fraley (1989) *Science* 244: 1293; Fisk and Dandekar, (1993) *Scientia Horticulturae* 55: 5;

Christou (1994) *Agro Food Industry Hi Tech*, p. 17; and the references cited therein).

Apomixis is a genetically controlled method of reproduction in plants where the embryo is formed without union of an egg and a sperm. There are three basic types of apomictic reproduction: 1) apospory where the embryo develops from a chromosomally unreduced egg in an embryo sac derived from the nucellus, 2) diplospory where the embryo develops from an unreduced egg in an embryo sac derived from the megaspore mother cell, and 3) adventitious embryony where the embryo develops directly from a somatic cell. In most forms of apomixis, pseudogamy or fertilization of the polar nuclei to produce endosperm is necessary for seed viability. In apospory, a "nurse" cultivar can be used as a pollen source for endosperm formation in seeds. The nurse cultivar does not affect the genetics of the aposporous apomictic cultivar since the unreduced egg of the cultivar develops parthenogenetically, but makes possible endosperm production.

Apomixis is economically important, especially in transgenic plants, because it causes any genotype, no matter how heterozygous, to breed true. Thus, with apomictic reproduction, heterozygous transgenic plants can maintain their genetic fidelity throughout repeated life cycles. Methods for the production of apomictic plants are known in the art. See, U.S. Patent No. 5,811,636 and references cited therein which are herein incorporated by reference.

The present invention also encompasses uniform populations of any of the plants discussed herein.

Successful transformation and plant regeneration have been achieved in the monocots as follows: asparagus (*Asparagus officinalis*; Bytebier et al. (1987) *Proc. Natl. Acad. Sci. USA* 84: 5345); barley (*Hordeum vulgare*; Wan and Lemaux (1994) *Plant Physiol.* 104: 37); maize (*Zea mays*;

Rhodes et al. (1988) *Science* 240: 204; Gordon-Kamm et al. (1990) *Plant Cell* 2: 603; Fromm et al. (1990) *Bio/Technology* 8: 833; Koziel et al. (1993) *Bio/Technology* 11: 194); oats (*Avena sativa*; Somers et al. (1992) *Bio/Technology* 10: 1589); orchardgrass (*Dactylis glomerata*; Horn et al. (1988) *Plant Cell Rep.* 7: 469); rice (*Oryza sativa*, including indica and japonica varieties; Toriyama et al. (1988) *Bio/Technology* 6: 10; Zhang et al. (1988) *Plant Cell Rep.* 7: 379; Luo and Wu (1988) *Plant Mol. Biol. Rep.* 6: 165; Zhang and Wu (1988) *Theor. Appl. Genet.* 76: 835; Christou et al. (1991) *Bio/Technology* 9: 957); rye (*Secale cereale*; De la Pena et al. (1987) *Nature* 325: 274); sorghum (*Sorghum bicolor*; Cassas et al. (1993) *Proc. Natl. Acad. Sci. USA* 90: 11212); sugar cane (*Saccharum* spp.; Bower and Birch (1992) *Plant J.* 2: 409); tall fescue (*Festuca arundinacea*; Wang et al. (1992) *Bio/Technology* 10: 691); turfgrass (*Agrostis palustris*; Zhong et al. (1993) *Plant Cell Rep.* 13: 1); and wheat (*Triticum aestivum*; Vasil et al. (1992) *Bio/Technology* 10: 667; Weeks et al. (1993) *Plant Physiol.* 102: 1077; Becker et al. (1994) *Plant J.* 5: 299).

Plant transformation vectors capable of delivering DNAs (genomic DNAs, plasmid DNAs, cDNAs, or synthetic DNAs) encoding plant-derived or other enzymes that affect the biosynthesis and accumulation of sterol compounds and tocopherols in plants for optimizing the pools of sitosterol, sitostanol, esters of either, and tocopherols, and for reducing the levels of campesterol, campestanol, and/or their esters, can be easily designed by art-recognized methods. Various strategies can be employed to introduce these encoding DNAs into plants to produce transgenic plants that biosynthesize and accumulate desirable levels of various sterol compounds and tocopherols, including:

1. Transforming individual plants with an encoding DNA of interest. Two or more transgenic plants, each containing one of these DNAs, can then be grown and cross-pollinated so as to produce hybrid plants containing the two DNAs. The
5 hybrid can then be crossed with the remaining transgenic plants in order to obtain a hybrid plant containing all DNAs of interest within its genome.

2. Sequentially transforming plants with plasmids containing each of the encoding DNAs of interest,
10 respectively.

3. Simultaneously cotransforming plants with plasmids containing each of the encoding DNAs, respectively.

4. Transforming plants with a single plasmid containing two or more encoding DNAs of interest.

15 5. Transforming plants by a combination of any of the foregoing techniques in order to obtain a plant that expresses a desired combination of encoding DNAs of interest.

Traditional breeding of transformed plants produced
20 according to any one of the foregoing methods by successive rounds of crossing can then be carried out to incorporate all the desired encoding DNAs in a single homozygous plant line (Nawrath et al. (1994) *Proc. Natl. Acad. Sci. USA* 91: 12760; PCT International Publication WO 93/02187), or to
25 produce hybrid offspring.

In methods 2 and 3, the use of vectors containing different selectable marker genes to facilitate selection of plants containing two or more different encoding DNAs is advantageous. Examples of useful selectable marker genes
30 include those conferring resistance to kanamycin, hygromycin, sulphonamides, glyphosate, bialaphos, and phosphinothricin.

C. Processes of Regeneration

Processes of regeneration of plants from transformed protoplasts are known in the art.

5 D. Transgenic Plants and Progeny

The present invention contemplates the plants that contain the exogenous constructs according to the present invention, such that a plant comprises at least one transformed plant cell comprising a nucleic acid construct.

10 The nucleic acid construct, as described above has as operably linked components in the 5' to 3' direction, a promoter, a DNA sequence encoding a polypeptide exhibiting 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity, and a transcription termination signal sequence.

15 The plant also comprises a nucleic acid construct that has as operably linked components in the 5' to 3' direction, a promoter, a DNA sequence encoding a steroid pathway enzyme, and a transcription termination signal sequence. The steroid pathway enzyme is a squalene epoxidase enzyme, a

20 sterol methyl transferase I enzyme, a sterol C4-demethylase enzyme, a obtusifoliol C14 α -demethylase enzyme, a sterol C5-desaturase enzyme, or a sterol methyl transferase II enzyme. In one embodiment, the nucleic acid constructs are recombinant constructs.

25 In one embodiment of the present invention a transgenic plant can be produced in accordance with the processes discussed elsewhere herein. One method to arrive at the above construct-containing plant is to transform the plant cell with a recombinant vector harboring such a construct.

30 Other methods involve direct transfer of the exogenous construct into the plant cell. The methods of arriving at a plant cell having exogenous nucleic acids are well known in art and are applicable to the present invention. In one embodiment, the nucleic acid constructs are recombinant

constructs. In a preferred embodiment, the recombinant vector is a plant expression vector.

The present invention contemplates a plant, the genome of which comprises introduced DNA. That introduced DNA has at least two components. One component is a DNA encoding a 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme. The other component is DNA encoding a steroid pathway enzyme that is a squalene epoxidase enzyme, a sterol methyl transferase I enzyme, a sterol C4-demethylase enzyme, a obtusifolioside C14 α -demethylase enzyme, a sterol C5-desaturase enzyme, or a sterol methyl transferase II enzyme. The storage organs, preferably seeds, of such a plant contain an elevated level of total accumulated sterol, compared to storage organs of an otherwise identical plant, the genome of which does not comprise the introduced DNA. The introduced DNAs are operatively linked to regulatory signals, preferably that cause seed-specific expression of said introduced DNAs. The seeds of such a plant contain a reduced level of squalene, cycloartenol, 24-methylene cycloartenol, obtusifolioside, stigmasterol-7-enol, or campesterol compared to the seeds of an otherwise identical plant or compared to a plant comprising an introduced DNA encoding a HMG CoA reductase enzyme without the contemplated steroid pathway enzyme.

Also contemplated is a plant with introduced DNA, as described above, that produces seed having an elevated level of a steroid pathway product, compared to a corresponding transgenic or non-transgenic plant that does not contain said introduced DNA.

The invention also contemplates a plant comprising introduced DNA encoding (i) an HMGR enzyme and (ii) a squalene epoxidase enzyme, a sterol methyl transferase I enzyme, a sterol C4-demethylase enzyme, a obtusifolioside C14 α -demethylase enzyme, a sterol C5-desaturase enzyme, a sterol

methy1 transferase II enzyme, or mixtures thereof, wherein said plant that produces a storage organ (preferably a seed) having an elevated level of a sterol pathway product compared to a corresponding transgenic or non-transgenic
5 plant that does not contain said introduced DNA.

The invention also contemplates a plant having introduced DNA, as described above, that produces a storage organ (preferably a seed) having a reduced level of squalene, cycloartenol, 24-methylene cycloartenol,
10 obtusifoliol, stigmasterol, campesterol, or mixtures thereof, compared to a corresponding transgenic plant that comprises introduced DNA encoding an HMGR enzyme but that does not contain introduced DNA encoding a squalene epoxidase enzyme, a sterol methyl transferase I enzyme, a
15 sterol C4-demethylase enzyme, a obtusifoliol C14 α -demethylase enzyme, a sterol C5-desaturase enzyme, a sterol methyl transferase II enzyme, or mixtures thereof.

For any of the above plants, an embodiment is contemplated wherein the introduced nucleic acid has
20 regulatory signals that cause seed-specific expression of said introduced DNAs.

The progeny of the above-described plants are also considered an embodiment of the present invention, as are plant cells or transformed plant cells. Cultures of those
25 plant cells are also contemplated. Plants produced from seeds having introduced DNA are also embodiments of the present invention.

A further embodiment of the present invention is a method of producing a plant that accumulates an elevated
30 level of sterol pathway products, in seed of said plant compared to seed of a corresponding plant comprising no introduced DNA encoding a peptide, polypeptide, or protein that affects the biosynthesis and accumulation of a sterol pathway product, comprising sexually crossing a plant having

introduced nucleic acid with the corresponding plant having no introduced DNA. Plants, including apomictic plants produced by this method are contemplated.

Another embodiment is a seed resulting from a cross of
5 a plant having introduced DNA, described above, with a nurse cultivar. Also contemplated are seeds of any of the above-described plants. Also part of the present invention plant parts, other than a seed of any of the above-described plants.

10 Uniform populations of the above-described plants are also contemplated.

E. Stability of Transgene Expression

As several overexpressed enzymes may be required to
15 produce optimal levels of substrates for the biosynthesis of sterol compounds and tocopherols, the phenomenon of co-suppression may influence transgene expression in transformed plants. Several strategies can be employed to avoid this potential problem (Finnegan and McElroy (1994)
20 *Bio/Technology* 12: 883).

One commonly employed approach is to select and/or screen for transgenic plants that contain a single intact copy of the transgene or other encoding DNA (Assaad et al. (1993) *Plant Mol. Biol.* 22: 1067; Vaucheret (1993) *C.R. Acad. Sci. Paris, Science de la vie/Life Sciences* 316: 1471;
25 McElroy and Brettell (1994) *TIBTECH* 12: 62). *Agrobacterium*-mediated transformation technologies are preferred in this regard.

Inclusion of nuclear scaffold or matrix attachment
30 regions (MAR) flanking a transgene has been shown to increase the level and reduce the variability associated with transgene expression in plants (Stief et al. (1989) *Nature* 341: 343; Breyne et al. (1992) *Plant Cell* 4: 463; Allen et al. (1993) *Plant Cell* 5: 603); Mlynarova et al.

(1994) *Plant Cell* 6: 417; Spiker and Thompson (1996) *Plant Physiol.* 110: 15). Flanking a transgene or other encoding DNA with MAR elements may overcome problems associated with differential base composition between such transgenes or
5 encoding DNAs and integrations sites, and/or the detrimental effects of sequences adjacent to transgene integration sites.

The use of enhancers from tissue-specific or developmentally-regulated genes may ensure that expression
10 of a linked transgene or other encoding DNA occurs in the appropriately regulated manner.

The use of different combinations of promoters, plastid targeting sequences, and selectable markers for introduced transgenes or other encoding DNAs can avoid potential
15 problems due to trans-inactivation in cases where pyramiding of different transgenes within a single plant is desired.

Finally, inactivation by co-suppression can be avoided by screening a number of independent transgenic plants to identify those that consistently overexpress particular
20 introduced encoding DNAs (Register et al. (1994) *Plant Mol. Biol.* 25: 951). Site-specific recombination in which the endogenous copy of a gene is replaced by the same gene, but with altered expression characteristics, should obviate this problem (Yoder and Goldsbrough (1994) *Bio/Technology* 12:
25 263).

Any of the foregoing methods, alone or in combination, can be employed in order to insure the stability of transgene expression in transgenic plants of the present invention.

30

F. Hybrid Plants

The invention contemplates a plant having introduced DNA encoding an HMGR and at least one of the six steroid pathway enzymes, as described in detail above. It is

contemplated that a transgenic plant having DNA encoding an HMGR, as is known in the art, might be crossed with a transgenic plant having DNA encoding at least one of the six steroid pathway enzymes.

5 Also contemplated as a hybrid plant according to the invention is a plant that is a hybrid of a transgenic plant having introduced DNA encoding an HMGR and at least one of the six steroid pathway enzymes wherein the plant has been hybridized with another strain, yet still retains the
10 introduced DNA.

G. Storage Organs

The term "storage organ" as used herein, refers to the seeds, fruits or vegetable parts of a plant. Most often the
15 seed is important for use in the present invention. However, there are consumable embodiments, such as with potatoes or carrots, where the vegetable parts are preferred.

A contemplated embodiment of the present invention is a
20 storage organ comprising at least one transformed host cell. The transformed host cell has at a minimum a construct according the invention as described above. Also contemplated are the embodiments when the construct has plant promoters, when the construct is recombinant, when the
25 construct is part of a vector, and when the vector is a plant expression vector.

The invention contemplates a transgenic plant seed transformed with a vector comprising a DNA segment that encodes a polypeptide having HMG-CoA reductase activity, and
30 a DNA segment that encodes a polypeptide having a steroid pathway enzyme, wherein the transgenic plant seed is capable of germinating into a transgenic plant that over-accumulates steroid pathway products relative to a native, non-transgenic plant of the same strain; and mutants,

recombinants, genetically engineered derivatives thereof and hybrids derived therefrom, wherein said mutants, recombinants, genetically engineer derivatives thereof and hybrids derived therefrom maintain the ability to
5 overaccumulate steroid pathway products.

Seed from a transgenic plant is grown in the field or greenhouse, and resulting sexually mature transgenic plants are self-pollinated to generate true breeding plants. The progeny from these plants become true breeding lines that
10 are evaluated for steroid compound or squalene accumulation, preferably in the field under a range of environmental conditions.

The commercial value of a transgenic plant with increased steroid compound or squalene accumulation is
15 enhanced if many different hybrid combinations are available for sale. The user typically grows more than one kind of hybrid based on such differences as time to maturity, standability or other agronomic traits. Additionally, hybrids adapted to one part of a country are not necessarily
20 adapted to another part because of differences in such traits as maturity, disease and herbicide resistance. Because of this, steroid compound or squalene accumulation is preferably bred into a large number of parental lines so that many hybrid combinations can be produced.

25 Adding an enhanced steroid compound or squalene accumulation trait to an agronomically elite line is accomplished by a variety of techniques well known to those of skill in the art. For example, parent transgenic plants that are either homozygous or contain a single independent
30 segregatable gene that encodes a polypeptide having HMG-CoA activity and thus for enhanced sterol or squalene accumulation are crossed with lines having other desirable traits such as herbicide resistance (U.S. Pat. No. 4,761,373) produce hybrids. Preferably, transgenic plants

homozygous for enhanced sterol or squalene accumulation are used to generate hybrids.

For example, a transgenic plant homozygous for enhance sterol accumulation is crossed with a parent plant having
5 other desired traits. The progeny, which are heterozygous or independently segregatable for enhanced sterol accumulation and their other desired traits. The backcrossing of progeny with the parent may have to be repeated more than once to obtain a transgenic plant that
10 possesses all desirable traits.

Alternatively, transgenic plants with an enhanced sterol or squalene accumulation trait are made multiply transgenic by introducing into such plants other genes that encode and express other desirable traits, or are mutated as
15 with radiation, e.g. X-rays or gamma rays, as in U.S. Pat. No. 4,616,099, whose disclosures are incorporated by reference. Thus, the present invention also contemplates mutants and genetically engineered derivatives of transgenic plants having enhanced sterol or squalene accumulation.

20 VI. Harvest

Besides seed, elevated levels of sterols, phytosterols, such as sitosterol, phytostanols, such as sitostanol, and esters thereof, can be found in other parts of the plants encompassed herein. While the seed-specific promoters
25 contemplated in the present invention function preferentially in seed tissues, expression in other plant parts can be expected, depending upon the specificity of the particular promoter. In this case, promoters functional in plant plastids are less desirable than those primarily
30 directing expression in the cellular cytosol, though it may be desirable to use promoters to drive expression of the recombinant constructs or expression cassettes disclosed herein in tissues and organs other than seeds. For example, elevated levels of sterols, phytosterols, etc., can be

expected in fruits, as well as vegetable parts of plants other than seeds. Vegetable parts of plants include, for example, pollen, inflorescences, terminal buds, lateral buds, stems, leaves, tubers, and roots. Thus, the present invention also encompasses these and other parts of the plants disclosed herein that contain elevated levels of desirable phytosterol, and phytostanol.

Of course, a significant effect of introducing into plants the coding sequences disclosed herein will be on the content of phytosterols/phytosteranols and their esters of seed oil. Therefore, additional aspects of the present invention include oil obtainable from the seed of the plants described herein, and methods for producing such plants and oil. Methods for extracting and processing seed oils are well known in the art.

Oils produced by the cells, plants, and methods disclosed herein are superior in phytosterol/phytostanol composition to conventional oils in a variety of ways. Oil of the present invention can contain an elevated level of at least one sterol, at least one phytosterol, at least one phytosterol ester, at least one phytostanol, at least one phytostanol ester, or mixtures thereof. Preferred compounds include sitosterol, sitostanol, and their esters.

Oil from seed of plants containing and expressing introduced DNA encoding a sterol methyltransferase II enzyme advantageously contains a reduced level of campesterol, at least one campesterol ester, campestanol, at least one campestanol ester, or mixtures thereof. The sterol methyltransferase II-encoding DNA can be introduced alone, or in combination with other introduced DNA sequences encoding enzymes affecting the biosynthesis of steroid compounds as discussed herein. Campesterol/campestanol and their esters are considered to be undesirable because they are readily absorbed in the intestine, while their safety in

the blood is unknown. Employing the plants and methods disclosed herein, one can obtain seed oil comprising about 0% to about 19%, preferably about 0% to about 12%, more preferably about 5% to about 9% campesterol, at least one
5 campesterol ester, campestanol, at least one campestanol ester, or mixtures thereof by weight of the total sterol compounds of the oil. (The levels of these compounds are difficult to express on a percent seed dry weight basis because different seeds contain different percentages of
10 these compounds expressed on this basis) These values represent a reduction of about 10% to about 100% in the amount of these compounds compared to those in conventional oils.

Introduction into plant cells of the enzyme-encoding
15 DNA sequences discussed above modifies the biosynthesis of sterol compounds carried out by the methods, and in the cells, plants, and seeds, disclosed herein. In particular, the expression of an HMG CoA reductase in conjunction with DNA sequences for a steroid pathway enzyme is expected to
20 result in alteration of the steroid pathway product profiles in oil as the enhanced steroid pathway throughput produces substrates for the enhanced enzyme activity. The novel phytostanol ester compositions, e.g., sitostanol ester compositions, thus produced constitute another aspect of the
25 present invention.

A. Harvest of Steroid Compounds

Methods for the derivation of steroid compounds from cells are well known in the art. The invention contemplates
30 the recovery of biosynthesized steroid compounds from the leaves and/or stems of plants, from plant seeds, from plant's vegetative organs, from callouses, and from cell cultures of plants, yeasts or eukaryotic cells.

Different sources of steroid compounds are preferred for various plants. For use as a food or a food component as discussed later, the steroid compounds need not be isolated or purified to 100 percent purity. Steroid
5 compound-enriched plants may be utilized directly.

For example, from tobacco or *Arabidopsis*, it may be preferable to extract a pulp of the leaves and stems. From tomato, potato, or corn, it may be preferable to use the tomato, potato or corn in the form of the familiar storage
10 organs that are typically consumed either directly, or a derivative thereof, such as tomato paste, potato flakes, vegetable oil and many more that are well known in the food science arts.

If desired, after cultivation, the transgenic plant is
15 harvested to recover the sterol or squalene product. This harvesting step can consist of harvesting a callus culture, the entire plant, or only the leaves, or roots of the plant. This step can either kill the plant or, if only a non-essential portion of the transgenic plant is harvested, can
20 permit the remainder of the plant to continue to grow.

In preferred embodiments, this harvesting step further comprises the steps of:

(i) homogenizing at least a sterol-containing
25 or a squalene-containing portion of the transgenic plant to produce a plant pulp and using the sterol-or squalene-containing pulp directly, as in dried pellets or tablets as where an animal food is contemplated; or

30

(ii) extracting the squalene or sterol(s) from the plant pulp with an appropriate solvent such as an organic solvent or by supercritical extraction [Favati, et al., J.

Food Sci. 53:1532 (1988) and the citations therein] to produce a sterol-or squalene-containing liquid solution or suspension; and

- 5 (iii) isolating the squalene or sterol(s) from the solution or suspension.

At least a portion of the transgenic plant is homogenized to produce a plant pulp using methods well known
10 to one skilled in the art. This homogenization can be done manually, by a machine, or by a chemical means as long as the transgenic plant portions are broken up into small pieces to produce a plant pulp. This plant pulp consists of a mixture of squalene or the sterol of interest, residual
15 amounts of precursors, cellular particles and cytosol contents. This pulp can be dried and compressed into pellets or tablets and eaten or otherwise used to derive the benefits, or the pulp can be subjected to extraction procedures.

20 The sterol or squalene can be extracted from the plant pulp produced above to form a sterol-or-squalene-containing solution or suspension. Such extraction processes are common and well known to one skilled in this art. For example, the extracting step can consist of soaking or
25 immersing the plant pulp in a suitable solvent. This suitable solvent is capable of dissolving or suspending the squalene or sterol present in the plant pulp to produce a sterol-or squalene-containing solution or suspension. Solvents useful for such an extraction process are well
30 known to those skilled in the art and included several organic solvents and combinations thereof such as methanol, ethanol, isopropanol, acetone, acetonitrile, tetrahydrofuran (THF), hexane, and chloroform as well as water-organic solvent mixtures. A vegetable oil such as peanut, corn,

soybean and similar oils can also be used for this extraction as can steam distillation.

A whole plant or callus culture with an added, exogenous structural gene for a polypeptide having HMG-CoA reductase activity is grown under suitable conditions for a period of time sufficient for squalene or sterols to be synthesized and accumulated. The sterol-squalene-containing plant cells, preferably in dried form, are then lysed chemically or mechanically, and the squalene or sterol is extracted from the lysed cells using a liquid organic solvent or steam distillation, as described before, to form a sterol- or squalene-containing liquid solution or suspension by usual means such as chromatography.

The squalene or sterol is isolated from the solution or suspension produced above using methods that are well known to those skilled in the art of squalene and sterol isolation. These methods include, but are not limited to, purification procedures based on solubility in various liquid media, chromatographic techniques such as column chromatography and the like.

The invention contemplates a sitosterol or sitostanol ester composition extracted from the seed of a transgenic plant of the invention. The invention also contemplates such a sitosterol or sitostanol ester wherein an esterifying fatty acid has 2 to 22 carbon atoms in the main chain.

B. Harvest of Oil

The novel biosynthetic composition of the oil in the transgenic plants is contemplated. Thus, the present invention contemplates oil containing at least one sterol pathway product, extracted from seed of a described transgenic plant. Preferably, sitosterol, at least one sitosterol ester, or mixtures thereof, comprise at least about 50% by weight of the total sterol compounds of the

oil. Preferably, sitosterol, at least one sitosterol ester, or mixtures thereof, comprise at least about 0.08% of the dry weight of a contemplated seed. Preferably, the oil has a reduced amount of squalene, cycloartenol, 24-methylene
5 cycloartenol, obtusifoliol, stigmasta-7-enol, campesterol, or mixtures thereof, compared to oil from a corresponding transgenic plant that does not contain introduced DNA encoding a squalene epoxidase enzyme, a sterol methyl transferase I enzyme, a sterol C4-demethylase enzyme, a
10 obtusifoliol C14 α -demethylase enzyme, a sterol C5-desaturase enzyme, a sterol methyl transferase II enzyme, or mixture thereof, and that reduction is in the range of from about 10% to about 100%.

Oil is extracted from transgenic plant seeds of the
15 present invention by method well known in the art. By way of example, oil can be extracted from plant seeds using extraction methods set forth above for harvesting sterols and squalene from transgenic plants. Alternatively, oil can be extracted from transgenic plant seeds by usually used
20 methods for obtaining seed oils such as by crushing the seeds to produce a pulp and then pressing the pulp to obtain oil. The pulp can also be extracted with appropriate solvents (e.g. benzene) to obtain the oil. *Industrial Chemistry: A Manual for the Student and Manufacturer*, ed. By A. Rogers
25 and A. B. Aubert, D. Van Nostrand Co., New York, pages 547-548 (1912).

C. Uses of Oil

As discussed in the "Description of Related Art,"
30 phytosterols such as sitosterol are beneficial for lowering serum cholesterol (Ling et al. (1995) *Life Sciences* 57: 195-206) and preventing cardiac disease. Tocopherols act as antioxidants, and play a major role in protecting cells from damage caused by free radicals (Halliwell (1997) *Nutrition*

Review 55: 44-60). As the amount of sitostanol in conventional vegetable and bran oils is low relative to that of other sterol compounds, the oils of the present invention are particularly useful for reducing the concentration of low density lipoprotein cholesterol in plasma.

Thus, further aspects of the present invention include the following:

Cholesterol-lowering compositions comprising the oils and sitostanol ester compositions disclosed herein. Such cholesterol-lowering compositions can take the form of, or be used in, foods, food products, processed foods, food ingredients, food additive compositions, or dietary supplements that contain oils and/or fats. Non-limiting examples include margarines; butters; shortenings; cooking oils; frying oils; dressings, such as salad dressings; spreads; mayonnaises; and vitamin/mineral supplements. Patent documents relating to such compositions include U.S. Patents 4,588,717 and 5,244,887, and PCT International Publication Nos. WO 96/38047, WO 97/42830, WO 98/06405, and WO 98/06714. Additional non-limiting examples include toppings; dairy products such as cheese and processed cheese; processed meat; pastas; sauces; cereals; desserts, including frozen and shelf-stable desserts; dips; chips; baked goods; pastries; cookies; snack bars; confections; chocolates; beverages; unextracted seed; and unextracted seed that has been ground, cracked, milled, rolled, extruded, pelleted, defatted, dehydrated, or otherwise processed, but which still contains the oils, etc., disclosed herein.

Food additive compositions of the present invention can be made by a method comprising obtaining oil containing a phytostanol or phytostanol ester selected from sitostanol, at least one sitostanol ester, or mixtures thereof, from cultured cells, or seeds of a plant, of the present

invention, and evenly distributing the oil or desired phytostanol compound in finely divided form throughout the food product or food additive composition to which it is added by dissolution or by suspension in an emulsion. For example, the oil or phytostanol compound can be dissolved in an edible solubilizing agent, or can be mixed with an edible solubilizing agent, an effective amount of a dispersant, and optionally, an effective amount of an antioxidant. Examples of useful edible solubilizing agents include, but are not limited to, monoglycerides, diglycerides, triglycerides, vegetable oils, tocopherols, alcohols, polyols, or mixtures thereof. Examples of useful antioxidants include, but are not limited to, tocopherols, such as α -tocopherol, ascorbic acid, inexpensive synthetic antioxidants, and mixtures thereof. Effective carriers for preparing emulsions or suspensions include water, alcohols, polyols, other edible compounds in which the oil or phytostanol compound is soluble or insoluble, and mixtures thereof. Examples of useful dispersants include, but are not limited to, lecithin, other phospholipids, sodium lauryl sulfate, fatty acids, salts of fatty acids, fatty acid esters, other detergent-like molecules, and mixtures thereof. Alternatively, the food additive composition can be made by a method comprising obtaining oil containing at least one tocopherol, and a phytostanol or phytostanol ester selected from sitostanol, at least one sitostanol ester, and mixtures thereof, from cultured cells, or seed of a plant, of the present invention, and mixing the oil with an edible solubilizing agent and an effective amount of a dispersant. Again, the edible solubilizing agent can include, but is not limited to, monoglycerides, diglycerides, triglycerides, vegetable oils, tocopherols, alcohols, polyols, or mixtures thereof, and the dispersant can include, but is not limited to, lecithin, other phospholipids, sodium lauryl sulfate,

fatty acids, salts of fatty acids, fatty acid esters, other detergent-like molecules, and mixtures thereof.

The cholesterol-lowering compositions can also take the form of pharmaceutical compositions comprising a
5 cholesterol-lowering effective amount of the oils or sitostanol ester compositions disclosed herein, along with a pharmaceutically acceptable carrier, excipient, or diluent. These pharmaceutical compositions can be in the form of a liquid or a solid. Liquids can be solutions or suspensions;
10 solids can be in the form of a powder, a granule, a pill, a tablet, a gel, or an extrudate. U.S. Patent 5,270,041 relates to sterol-containing pharmaceutical compositions.

Any of the foregoing cholesterol-lowering compositions can be used alone or in combination in methods to lower the
15 risk of developing an elevated plasma concentration of low density lipoprotein cholesterol, to lower the plasma concentration of low density lipoprotein cholesterol, or to treat or prevent an elevated plasma concentration of low density lipoprotein cholesterol. Such methods comprise
20 orally administering to a human or animal subject an effective amount of cholesterol-lowering composition. What constitutes an effective amount of cholesterol-lowering composition can be determined empirically, and depends in part on a variety of factors, including the age, weight,
25 sex, diet, general medical condition of the subject, and the severity of hypercholesterolemia. Subjects undergoing treatment with the cholesterol-lowering combinations disclosed herein can be monitored by routine measurement of serum cholesterol levels to determine the effectiveness of
30 therapy. Continuous analysis of the data obtained in this way permits modification of the treatment regimen during therapy so that optimal effective amounts of the cholesterol-lowering compositions of this invention are administered, and so that the duration of treatment can be

determined as well. In this way, the treatment regimen/dosing schedule can be rationally modified over the course of treatment so as to achieve the lowest cholesterol-lowering effective amount of the present compositions which results in satisfactory anti-cholesterolemic effectiveness, and so that administration of these compositions is continued only so long as is necessary to successfully treat this condition. In general, an effective amount of a cholesterol-lowering composition of the present invention in the form of a phytostanol- or phytostanol ester-containing composition is in the range of from about 0.1 gm/day to about 4.5 gm/day. By way of example, a phytostanol ester composition, for example a sitostanol ester composition, can be administered in an amount in the range of from about 0.1 gm/day to about 4.5 gm/day, preferably from about 1 gm/day to about 4.5 gm/day, more preferably from about 2 gm/day to about 4.5 gm/day. A phytostanol composition, for example a sitostanol composition, can be administered in an amount in the range of from about 0.1 gm/day to about 3 gm/day, preferably from about 1 gm/day to about 3 gm/day, more preferably from about 2 gm/day to about 3 gm/day.

The cholesterol-lowering compositions of the present invention can be administered daily to patients in accordance with a number of different regimens. Fundamentally, these compositions should be administered in a cholesterol-lowering effective amount for a period of time effective to exert their anti-hypercholesterolemic preventing, reducing, or reversing action. Administration of the present cholesterol-lowering compositions should be continued until the hypercholesterolemic condition has been controlled or eliminated.

Another method encompassed by the present invention is that of achieving or improving effective absorption of sitostanol into a host, comprising producing at least one

sitostanol ester by any of the methods disclosed herein, and administering this sitostanol ester to a host, which can be a human or animal. The sitostanol ester can be administered by a route selected from oral route, parenteral route, or
5 topical route. The dose, which can be administered daily, can be up to about 10 milligrams of the sitostanol ester per kilogram of body weight. U.S. Patent 5,202,045 relates to the use of stanol fatty acid esters to reduce serum cholesterol.

10 Also envisioned are plants which in addition to having increased levels of phytosterols and phytostanols due to the presence of constructs comprising sequences encoding 3-hydroxy-3-methylglutaryl-Coenzyme A reductase and at least one other sterol synthesis pathway enzyme, have increase
15 levels of tocopherol due to the presence of constructs comprising sequences allowing the overexpression of enzymes in the tocopherol biosynthetic pathway.

Tocopherol levels vary in different plants, tissues, and developmental stages, indicating a highly regulated
20 biosynthetic pathway. The production of homogentisic acid by *p*-hydroxyphenylpyruvate dioxygenase is likely to be a regulatory point for bulk flow through the pathway because of irreversible enzyme action and because homogentisic acid production is the first committed step in tocopherol
25 biosynthesis (Norris et al., 1995, *Plant Cell* 7: 2139-2149). The other key regulatory step in tocopherol biosynthesis is the availability of the phytylpyrophosphate pool. Feeding studies (Furuya et al., 1987, *Phytochem.*, 26: 2741-2747) in safflower callus culture demonstrated 1.8-fold and 18-fold
30 increases in tocopherol synthesis by feeding homogentisate and phytol, respectively. In meadow rescue leaf, vitamin E increases in the initial phase of foliar senescence when phytol is cleaved off from the chlorophylls and when free phytol is available (Pesquier et al., 1989, *J. Plant Physiol.*

135: 428-432). These reports suggest tight coupling of tocopherol biosynthesis to the availability of homogentisic acid and phytol.

Transformation of plants with nucleic acid constructs
5 that increase the biosynthetic activity of the tocopherol pathway can lead to increased production of particular tocopherol isomers, for example, α -tocopherol, are known in the art and can be found, for example, in PCT International publication WO 00/61771 which is incorporated herein by
10 reference. Formation of α -tocopherol from other tocopherols occurs due to S-adenosylmethionine (SAM)-dependent methylases such as γ -tocopherol methyl transferase. Overexpression of methyl transferases in combination with 3-hydroxy-3-methylglutaryl-Coenzyme A reductase and at least
15 one other sterol synthesis pathway enzyme as described herein is also contemplated in the present methods. Thus, any of the DNAs encoding enzymes of the tocopherol biosynthetic pathway, discussed above, are useful in the present invention. Transformation of plants with an early
20 tocopherol biosynthesis gene is sufficient to produce plants having an elevated level of tocopherols. By "early tocopherol biosynthesis gene" is meant DNA encoding geranylgeranylpyrophosphate synthase, geranylgeranylpyrophosphate hydrogenase, 4-
25 hydroxyphenylpyruvate dioxygenase, and phytyl/prenyl transferase. DNA encoding enzymes active in later steps of tocopherol biosynthesis ("secondary tocopherol biosynthesis genes") can be expressed to enhance carbon flux through the tocopherol pathway even further, and to produce specific
30 tocopherol isomers. In this way, the tocopherol biosynthetic pathway can be modified to enhance production of any tocopherol compound of interest, such as α -tocopherol. As noted above, a variety of sources are

available for the early tocopherol biosynthesis genes (and other tocopherol biosynthesis genes), and a gene from any of these sources can be utilized. If co-suppression occurs when a plant gene native to the target host plant is used to increase expression of a particular enzyme, a coding sequence from another source can be used as an alternative.

Preferred genes for introduction into plants to alter tocopherol quantity/quality include 3-deoxy-D-arabino-heptulosonate-7-P synthase (DAHP synthase), shikimate kinase, either or both of the prephenate dehydrogenases, 1-deoxy-d-xylulose 5-phosphate synthetase (DXS), 1-deoxy-d-xylulose 5-phosphate reductoisomerase (DXR), 4-diphosphocytidyl-2C-methyl-d-erythritol synthase (YgbP), 4-diphosphocytidyl-2C-methyl-d-erythritol kinase (YchB), 2C-methyl-d-erythritol 2,4-cyclodiphosphate synthase (YgbB), the gene product of GcpE, LytB (Altincicek et al., 2001, *J. Bacteriol.*, 183:2411-2416; Altincicek et al., 2001, *J. Immunol.*, 166:3655-3658; Campos et al., 2001, *FEBS Lett.*, 488:170-173), geranylgeranylpyrophosphate synthase (GGPPS), geranylgeranylpyrophosphate hydrogenase (GGH), phytyl/prenyltransferase (PPT), 4-hydroxy-phenylpyruvate dioxygenase (HPPD), 2-methyl-6-phytylplastoquinol tocopherol methyltransferase I (MTI), tocopherol cyclase, γ -tocopherol methyltransferase (GMT) a plant *slr 1736* gene (see Cyanobase <http://www.kazusa.or.jp/cyanbase>), a plant *slr 1737* gene (see Cyanobase <http://www.kazusa.or.jp/cyanbase>), an *ATPT2* gene (Smith et al., *Plant J.*, 11:83-92, 1977), and an *AANT1* gene (Saint Guily et al., *Plant Physiol.*, 100:1069-1071, 1992).

4-hydroxy-phenylpyruvate dioxygenase and geranylgeranylpyrophosphate hydrogenase will increase the homogentisate and phytol pools, respectively. Enzymes that control fluxes through pathways are well known to be regulated in higher organisms such as plants. Therefore, 4-hydroxyphenylpyruvate dioxygenase and

geranylgeranylpyrophosphate hydrogenase genes of microbial origin which are not subject to regulation in plants, or those from higher organisms (plants, algae, fungi, etc.) that are deregulated, are especially attractive in this regard. A non-limiting example is the microbial enzyme 4-amino-4-deoxyprephenate dehydrogenase (TyrA from *Erwinia herbicola*) which can replace prephenate aminotransferase, arogenate dehydrogenase and aminotransferase. Overexpression of enzymes such as 3-deoxy-arabino-heptulosonate 7-P (DAHP) synthase, prephenate dehydrogenase, and shikimate kinase would lead to increases in the levels of homogentisate. DNA encoding any of the tocopherol biosynthetic enzymes discussed herein can be introduced alone or in various combinations to enhance tocopherol quantity and/or alter tocopherol quality. When introduction of multiple enzymes is desirable, preferred combinations include, but are not limited to, 4-hydroxyphenylpyruvate dioxygenase (HPPD) plus geranylgeranylpyrophosphate hydrogenase (GGH), geranylgeranylpyrophosphate synthase (GGPP synthase) plus geranylgeranylpyrophosphate hydrogenase (GGH), 4-amino-4-deoxyprephenate dehydrogenase (TyrA) plus phytylprenyltransferase (PPT), geranylgeranylpyrophosphate hydrogenase (GGH) plus phytylprenyltransferase (PPT), geranylgeranylpyrophosphate synthase (GGPP synthase) plus phytylprenyltransferase (PPT), 2-methyl-6-phytylplastoquinol tocopherol methyltransferase I (MTI) plus phytylprenyltransferase (PPT), or 2-methyl-6-phytylplastoquinol tocopherol methyltransferase I (MTI), phytylprenyltransferase (PPT), 4-hydroxyphenylpyruvate dioxygenase (HPPD) and geranylgeranylpyrophosphate synthase (GGPP synthase).

Plants characterized by increase levels of sterol and tocopherol production can be produced by transforming plant cells or tissues genetically altered for increased sterol

production by the methods described herein with additional nucleic acid constructs encoding tocopherol biosynthetic enzymes. Introduction of constructs encoding tocopherol pathway enzymes can be accomplished using standard methods in molecular biology such as those described herein or those described in PCT International Publication WO 00/61771. Introduction of constructs encoding 3-hydroxy-3-methylglutaryl-Coenzyme A reductase, at least one other sterol synthesis pathway enzyme, and at least one tocopherol synthesis pathway enzyme can be accomplished in a single transformation or in a series of transformations. For example, and without limitation, plant cells transformed with constructs encoding 3-hydroxy-3-methylglutaryl-Coenzyme A reductase, at least one other sterol synthesis pathway enzyme as described herein could be selected and then further transformed with additional constructs encoding one or more tocopherol synthesis pathway enzymes and in particular S-adenosylmethionine-dependent γ -tocopherol methyltransferase enzyme. Successfully transformed cells can then be selected and used to regenerate plants having increased levels of phytosterols and/or phytostanols as well as increased levels of tocopherol. Plants produced can then be "selfed", a technique well known in the art, to produce uniform populations of plants.

Alternatively, plants characterized by increased levels of tocopherols and phytosterols and/or phytostanols can be produced by traditional plant breeding methods. For example, plants transformed with nucleic acid constructs encoding 3-hydroxy-3-methylglutaryl-Coenzyme A reductase and at least one other sterol synthesis pathway enzyme can be sexually crossed with high tocopherol plants. Any plant transformed to produce increased levels of tocopherols and in particular α -tocopherols can be used. Non-limiting

examples include plants produced by the methods described above and in PCT International publication WO 00/61771.

If desired, the plants produced can be selfed to produce homozygous, uniform populations of plants.

5 Seed obtained from the transgenic, progeny, hybrid, etc., plants disclosed herein can be used in methods for obtaining oil containing phytosterols, phytosterol esters, phytostanols, phytostanol esters, or mixtures thereof along with tocopherols employing extraction and processing
10 procedures known in the art. Note, in this regard, Kochhar (1983) *Prog. Lipid Res.* 22: 161-188. Alternatively, seeds with increased levels of tocopherols and phytosterols, phytosterol esters, phytostanols, phytostanol esters, or mixtures thereof; or fruits and vegetables with increased
15 levels of tocopherols and phytosterols, phytosterol esters, phytostanols, phytostanol esters, or mixtures thereof, can be used directly.

Tocopherols and phytosterols and/or phytostanols can then be obtained from deodorized distillates of oil seed
20 extracts and in particular soybean oil extracts. Such deodorized distillates are expected to contain increased levels of both tocopherols and phytosterols and/or phytostanol extracts. Oil extracts from plants and seed of the present invention are particularly valuable in that they
25 allow the production of high sterol/tocopherol oils in a single process thus resulting in reduced purification costs, processing time and waste stream. Methods for the isolation of tocopherols and sterols from plant oils are well known in the art and can be found, for example, in U.S. Patent Nos.
30 4,454,329; 5,097,012; 5,594,437; and 5,981,781.

EXAMPLES

The following examples are intended to provide illustrations of the application of the present invention.

The following examples are not intended to completely define or otherwise limit the scope of the invention.

Example 1. Enhancement of Phytosterol content in seeds of transgenic plants by seed-specific overexpression of
5 full-length HMG-CoA reductase (HMGR)

In order to examine the ability of HMGR overexpression for increasing sterol compound levels in seeds, the following experiment was performed in *Glycine max*. A full-length HMGR gene from rubber genomic DNA was expressed in
10 developing *Glycine max* seeds using the 7S promoter. This was achieved by excising the rubber HMGR gene from the plasmid pHEV15 (Schaller et al., (1995) *Plant Physiol.*, 109: 761-770) using *EcoRI*. The 3.8 Kb fragment was inserted into the *EcoRI* site of pMON29920 (Fig. 3) such that the HMGR gene is
15 flanked by the 7S promoter on the 5' end and the E9 3' terminator to create pMON43800 (Fig. 4). This was next digested with *SalI* and *NotI* to release a 7.7 Kb fragment that was then blunt-ended at the *SalI* end before ligating to pMON23616 (Fig. 5) that was first cut with *SmaI* and *NotI*.
20 This created the pMON43818 binary vector that contains the rubber HMGR gene driven by 7S promoter and the NPTII gene selection marker driven by the NOS promoter and 3' NOS terminator. pMON43818 (Fig. 6) was used to transform *Agrobacterium tumefaciens* and transform *Glycine max*
25 cotyledon explants as described in Example 2.

Seeds from 15 transgenic plants and one nontransgenic control plant were harvested at maturity. Sterol extraction and analysis on ten individual seeds per plant were performed as described in Example 2. Results are presented
30 in Table 2.

Event	Campesterol	Stig- asterol	Sitosterol	Sito- tanol	Others (Pathway intermediates)	Total	Inter- mediate accumul- ation
	ug/g	ug/g	ug/g	ug/g	ug/g	ug/g	(% of total sterol)
1	161.9	148.2	551.3	36.8	264.8	1163	22.8
2	241.6	287.9	1128.8	96.6	1489.8	3244.5	46
3	442.4	320.1	1876.6	117.3	1728.4	4484.8	38.5
4	311.2	345.6	1645.6	113.8	1307.5	3723.6	35
5	395.5	323.0	1592.1	83.1	933.8	3327.5	28
6	370.5	301.6	1735.8	97.2	990.5	3495.6	28.3
7	351.0	307.0	1457.3	101.1	885.3	3101.7	28.5
8	248	172.4	1270.1	74.3	428.8	2193.6	19.5
9	221.1	140.7	1149	76.7	652.6	2240.1	29.1
10	234.2	184.8	1306.8	64.1	669.4	2459.3	27.2
11	156.5	125.4	679.2	38.8	142.3	1142.2	12.4
12	311.2	242.9	1457.3	67	418.6	2497	16.7
13	165.4	135.4	1320.1	59.7	1645.8	3326.4	49.4
14	190.8	152	1121.3	51.4	1040.7	2556.2	40.7
15	182.9	157.4	1118.5	55.2	376.6	1890.6	20
16	197.9	151.7	946.6	61.7	225.3	1583.2	14.2

Table 2: Sterol profile of transgenic soybean plants expressing rubber HMGR gene driven by 7s promoter. Event 5 1:control, events 2-16:15 transgenic plants generated by 15 independent events using *Agrobacterium* mediated transformation.

Total sterols increased by 3.2- and 3.9- fold in the best performing plants (transgenic events 3 and 4). These 10 two events also showed the highest increases of individual sterols. Campesterol increased by 2.7-fold, sitosterol by 3.4-fold, sitostanol by 3.2-fold and other sterols by 6.5-fold in event 3 while stigmasterol increased by 2.3-fold in event 4. The other sterols, which account for the highest 15 increase in total sterols were pathway intermediates that included squalene, cycloartenol, 24-methylene cycloartenol, obtusifolliol, isofucosterol, and stigmasta-7-enol. These pathway intermediates normally form minor constituents in the sterol composition of seeds. However, in the transgenic

seeds, probably due to increased carbon flux through the pathway, they accumulate in significant amounts. This suggests additional control points for sterol biosynthesis in plants such as squalene epoxidase, C-24 sterol methyltransferase, and C-14 obtusifoliol demethylase.

Example 2: Enhance phytosterol biosynthesis in seeds of transgenic soybean plants by seed-specific expression of catalytic domain of HMG-CoA Reductase (HMGR) alone and in combination with sterol methyl transferase II (SMTII)

In another embodiment of the present invention, the levels of sterol compounds, including sitosterol, sitostanol, campesterol, stigmasterol and at least one ester for each of the sterol compounds and mixture thereof, can be elevated in plant seeds by overexpression of catalytic domain of plant-HMG-CoA reductases. One can transform a plant of interest using an expression cassette or vector comprising DNA encoding a polypeptide exhibiting 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMG-CoA reductase or HMGR) activity. HMGR cDNAs from rubber have been successfully used to increase plant sterol levels in plant tissues (Schallet et al. (1995) *Plant Physiol.* 109: 761-770). Full-length and truncated forms of HMGR CDNAs encoding full-length and catalytic domain of HMGR, respectively, from *Arabidopsis* have also been used to overproduce sterols in transgenic *Arabidopsis* plants (Gonzalez et al. (1997) *Third Terpenet Meeting of the European Network on Plant Isoprenoids Abstracts*, Abstract No. 33, page 33). In the above examples however, the genes have not been specifically targeted to increase sterol levels in seeds. Another approach to enhance the nutritionally beneficial 24-ethyl sterols (sitosterol, sitostanol) and reduce the accumulation of 24-methyl sterols (campesterol) in seeds one can co-express two genes encoding

the enzymes HMGR and sterol methyl transferase II (SMTII), each under the control of seed-specific promoter. Here we present evidence for such approaches: sterol composition of transgenic soybean seeds harboring truncated form (catalytic domain of HMGR without linker) of *Arabidopsis* HMGR1 is presented in Figure 11 and Table 3. Sterol composition of transgenic soybean seeds harboring *Arabidopsis* HMGR1 (catalytic domain of HMGR without linker) and *Arabidopsis* SMTII is presented in Figure 12 and Table 4.

In order to examine whether overexpression of the catalytic domain of HMGR increases sterol levels in the seeds of transgenic soybean, the following experiment was performed in *Glycine max*. A truncated form of HMGR1 cDNA encoding only the catalytic domain of HMGR from *Arabidopsis* was expressed in developing seeds of *Glycine max* using the seed-specific 7S promoter. This was achieved by excising the cDNA fragment (HMGR1cd) encoding the HMGR1 catalytic domain from the plasmid pHMGR1cd (Dale et al., (1995) Eur. J. Biochem. 233: 506-513) using NdeI and SmaI enzymes resulting in the isolation of a 1.9 Kb fragment. The NdeI overhang was filled-in and the 1.9 Kb fragment was blunt-end ligated to vector pMON43818 (Figure 6), previously XhoI (XhoI overhang was filled-in) and SmaI digested such that the HMGR1cd was flanked by the 7S promoter on the 5' end and the E9 3' terminator to create a recombinant vector pMON43052 (Figure 7). This was next digested with XbaI and blunt-ended and then digested with NotI to release a 3.4 Kb fragment and ligated to pMON51850 (Figure 8) that was digested with SmaI and NotI. The ligation created a recombinant binary vector pMON43057 (Figure 9) that contained the cDNA fragment encoding the catalytic domain of *Arabidopsis* HMGR1, driven by 7S promoter and E9 3' terminator and the NPTII selectable marker gene driven by the NOS promoter and 3' NOS terminator. The pMON43057 was

used for *Agrobacterium tumefaciens* mediated transformation of *Glycine max* cotyledon explants. The pMON43058 (Figure 10) construct carrying both the catalytic domain of *Arabidopsis* HMGR1 and *Arabidopsis* SMTII, both driven by the 7S promoter, was also used for *Agrobacterium tumefaciens*-mediated transformation of *Glycine max* in a similar manner described below.

Explants for transformation were prepared as follows: sterilized seeds were germinated on germination medium under light at 28°C for 5-6 days. Germinated seeds were placed in the dark at 4°C for 24 hours prior to excision. Seed coats were removed and hypocotyls of each seedling trimmed to a length of 0.5 cm to 1.0 cm in length. The cotyledons were then split open such that the hypocotyl was split down in the middle. The primary leaves and apical region of each cotyledon was removed to expose the wounding region. Wounding was performed with 3-7 shallow, scalpel scores in line with the embryo axis, ensuring that the apical bud was damaged. Wounded explants were incubated in the culture of *Agrobacterium tumefaciens* containing pMON43057. Incubation was for 1 hour at room temperature. Inoculated explants were then transferred to a co-culture medium and placed under light at 23°C for 3-4 days. At this time explants were transferred to shooting medium without kanamycin selection and placed in a 25°C light growth room for 4 days.

After 4 days on delay, explants were transferred to a 186 ppm kanamycin selection medium and placed in a 25°C light growth room for 2 weeks. At the end of two weeks explants were transferred to 186 ppm Woody Plant medium and placed again in a 25°C light growth room for another 2 weeks. Cultures were transferred every 2 weeks to fresh medium for approximately 18-21 weeks. At the 6 week transfer, the cotyledons and any dead material were removed from the explants, and the petiole was cut. At each subsequent 2

week transfer, the petiole was cut to expose fresh cells to the medium.

Transgenic shoots that were approximately ½" in length, with 2 nodes, 1 open trifoliate and an active growing point were selected, cut and transferred to rooting medium. Once a good root system was developed, the plants were sent to the greenhouse to grow up in soils in pots.

Seeds from the 15 transgenic plants and one nontransgenic control plant were harvested at maturity. Ten individual seeds from each plant were weighed and ground into fine powder using an electric grinder. A known amount of cholestane (usually 100µg in 100µl ethanol) was added to each approximately 50mg powder sample. Sterol compounds were hydrolyzed directly from the ground tissue by saponification with 2ml of 10% KOH in methanol by refluxing the material at 60°C for 30 minutes. The refluxed samples were cooled to room temperature and filtered through glass wool. An equal volume of water was added to each filtrate, and the nonsaponifiables were extracted by partitioning three times with equal volumes of hexane. The hexane phases were pooled and evaporated. The residues were resuspended in 1 ml of acetone, and quantitatively transferred to glass GC vials that were immediately capped. Sterols were analyzed by Gas Chromatography-Flame Ionizing Detector using the following conditions: Inlet temperature of 220°C, detector temperature of 320°C, and column oven temperature programmed from 220°C to 320°C with initial temperature for 1 minute and final temperature for 16 minutes and ramp rate of 8°/min. The column used was a glass capillary DB-5 column of 50 m length, 320 µm diameter, and a film thickness of 0.25 µm. The carrier gas was helium at a flow rate of 1.0ml/min. Results are presented in Table 3 and Table 4.

Source	Unknown 1 µg	Compensated µg	Biogenical µg	Unknown 2 µg	Observed µg	Basilar µg	Scalard µg	Isolated µg	Sigmast-7, µg	Unknown 3 µg	Cyclanid µg	74 Methylene Cyclanid µg	Total used µg	Total End Product µg	Total Intensities µg	Total Etyl Sterol µg	Total Etyl Sterol µg	Ratio of methylene µg	Total Unknowns µg	% Intensities (of Total Sterol)	C ₁₇ d	Esterified Compound	Esterified C ₁₇ d
2070	18	160	142	88	54	1046	33	147	871	137	232	532	5356	2112	3001	2089	160	242	56				
2155	168	1378	1516	0.0	0.0	547.1	34.6	13.9	31.6	34.0	30.3	47.8	1081.9	922.1	123.4	134.6	119.5	31.5	41.4	11.2			
2185.2	11.7	1089	130.4	88.4	82.3	888.9	40.3	164.0	600.4	273.0	374.6	483.9	5710.0	2037.4	3222.3	2107.0	119.5	389.7	37.4				
2262.0	11.6	1089	130.4	88.4	11.9	972.6	38.9	118.0	718.4	138.9	166.4	479.3	5004.0	2016.5	3210.1	1856.1	149.0	247.4	35.6				
2282.3	20.1	1124.3	140.0	89.7	84.2	1118.0	75.0	164.3	676.8	210.9	203.8	521.4	5719.8	2121.8	3216.6	2169.0	178.3	300.4	36.0				
1881.3	18.1	200.4	170.3	65.3	71.7	1237.7	68.1	123.8	862.3	63.8	232.2	684.4	5331.1	2121.8	2400.3	1690.1	200.4	0.08	187.9	37.2			
2432.0	33.5	123.5	153.6	78.9	75.6	1382.4	44.7	161.3	800.6	921.3	321.6	441.0	5317.3	1691.3	3122.7	1690.1	151.5	0.08	213.3	82.0			
2244.6	2.2	146.7	120.8	41.3	86.3	1150.0	42.6	120.3	516.6	188.2	202.2	411.3	5269.0	2059.1	3043.2	1882.6	160.7	0.07	212.7	37.8			
2038.8	6.2	1331.6	152.1	41.5	81.2	837.7	13.7	210.5	102.7	35.3	222.7	318.9	4033.2	1648.1	3278.9	1127.7	134.8	0.12	106.2	71.4			
2105.1	13.6	127.1	131.7	85.7	64.7	1100.9	80.7	161.1	935.0	173.7	242.1	933.3	5644.6	2447.4	3232.2	2091.4	137.1	0.05	275.0	54.2			
1845.9	11.0	163.7	116.7	89.0	80.1	1024.4	89.5	137.6	89.8	209.9	270.3	481.1	5165.0	2046.6	3359.8	2650.1	145.7	0.07	281.6	55.1			
1876.4	31.3	189.7	176.4	95.9	93.5	1377.6	39.8	124.2	618.8	218.2	266.7	372.8	5475.0	2259.8	3728.8	2684.2	108.7	0.09	305.5	53.1			
2393.0	7.6	138.6	160.5	86.7	110.6	1470.1	88.0	140.2	810.2	278.1	278.1	1018.6	7133.1	2811.1	4033.0	2001.6	156.6	0.05	368.0	55.3			
1328.8	21.6	182.1	170.0	78.5	47.0	1622.5	89.7	116.1	572.8	138.0	317.7	455.7	4534.3	2035.7	2163.7	1959.5	192.2	0.10	216.1	49.8			
830.9	7.4	170.8	110.7	41.6	35.6	607.0	34.6	88.1	603.7	61.8	131.6	301.5	3202.2	1531.5	1515.1	1468.9	170.8	0.12	135.4	47.3			
2432.9	0.0	186.3	141.6	74.0	86.2	1420.5	50.4	164.2	1016.6	171.3	326.3	1035.3	7113.1	2161.1	4088.6	2813.8	156.3	0.05	334.2	57.4			
1875.1	17.0	182.3	133.8	71.2	21.6	1868.2	42.2	145.2	818.3	193.4	218.2	482.4	5016.7	2161.1	2740.2	2059.0	162.3	0.05	274.4	54.3			
1740.1	18.8	133.4	137.6	73.1	20.1	831.1	81.1	121.7	638.4	178.7	342.3	364.7	4988.6	1818.9	2611.8	1607.2	132.4	0.07	270.8	56.2			
1864.4	31.1	115.1	130.9	57.1	41.0	1108.0	91.4	113.0	717.9	100.1	443.6	488.8	3240.0	2083.4	3320.3	2217.7	152.9	0.07	217.2	55.5			
1817.3	21.6	182.5	132.4	34.4	38.6	1227.2	70.3	132.7	801.2	107.8	212.8	409.4	4408.2	2017.3	2405.2	1919.1	162.1	0.04	185.6	52.2			
2013.5	16.7	181.0	120.1	61.6	37.4	1304.9	84.3	126.3	739.7	40.0	225.9	391.2	4863.7	2123.8	2652.9	2061.0	102.3	0.09	206.9	53.3			
2125.9	16.1	135.1	126.0	80.2	75.1	1111.6	77.4	160.3	693.2	261.8	350.3	511.2	2177.8	2177.8	2497.0	2354.2	151.9	0.09	152.5	54.1			
2348.9	16.6	184.3	128.0	29.1	38.0	912.6	80.6	78.9	428.8	110.0	112.2	308.9	4647.6	2113.6	4035.7	2369.0	112.1	0.06	268.1	60.7			
1181	17	173	136	40	31	911	42	65	268	93	314	318	4628.6	1865.7	2162.9	1574.6	144.3	0.10	158.7	60.8			
2070	18	160	142	88	54	1046	33	147	871	137	232	532	5356	2112	3001	2089	160	242	56				

To fully characterize the sterol compounds present in the transgenic seeds, a representative sample was also analyzed by Gas Chromatography-Mass Spectrometry (GC-MS) for confirmation of the sterol compounds present. The GC-MS conditions were as follows: inlet temp. 250°C, detector 320°C, oven programmed from 180°C to 325°C with initial equilibration time of 1.0 min, ramping to 310°C at 4°/min at then 20°/min to 325°C. The column was a DB-5 capillary glass column similar to the one used for GC-FID.

Majority of the transgenic lines harboring pMON43057 showed 3 to 5-fold increase in total sterols. The best performing transgenic lines, GM_A13342 and GM_A13634, showed 6.5- and 6.1-fold increase in total sterols, respectively. These lines showed 2- to 2.6-fold increase in sitosterol, 1.5 to 2.2-fold increase in sitostanol and no significant change in the campesterol levels. Hence the major proportion of the total sterol increase was accounted by the accumulation of pathway intermediates which include squalene, cycloartenol, 24-methylene cycloartenol, obtusifoliol, isofucosterol, and stigmasta-7-enol. The best performing transgenic lines, GM_A13342 and GM_A13634, showed 32.6- and 32.2-fold increase in pathway intermediates accumulation, respectively, as compared to the control. In all the transgenic lines harboring the pMON43057, 50-70% of the total increase was accounted by the increase in the pathway intermediates accumulation as compared to the control. The pathway intermediates include squalene, cycloartenol, 24-methylene cycloartenol, obtusifoliol, isofucosterol, and stigmasta-7-enol.

Six transgenic lines harboring pMON43058 produced 5.8- to 6-fold increase in total sterols and the rest of the 10 transgenic lines with the pMON43058 showed 3- to 5-fold increase in total sterols. The best performing transgenic lines showed about 2- to 3-fold increase in sitosterol and

4.5- to 6-fold increase in sitostanol levels. However, the campesterol accumulation was reduced by 50% in these lines. This was due to overexpression of the *Arabidopsis* SMTII enzyme which enhances the carbon flux towards the synthesis of 24-ethyl sterols thereby reducing the carbon flux through the pathway leading to the synthesis of 24-methyl sterols. As seen in pMON43057 transgenic lines, all of the transgenic lines harboring the pMON43058 also accumulated 50-60% of the total sterols in the form of pathway intermediates which are squalene, cycloartenol, 24-methylene cycloartenol, obtusifoliol, isofucosterol, and stigmasta-7-enol. These pathway intermediates normally form minor constituents in the sterol composition of seeds. However, in the transgenic seeds, probably due to increased carbon flux through the pathway, they accumulate in significant amounts. The pathway intermediates accumulation is highly significant when the truncated form of HMGR is overexpressed as compared to the full length form of HMGR suggesting that the overexpression of the truncated form of HMGR creates even greater increase in carbon flux through the pathway. This provides further evidence for additional control points for sterol biosynthesis in plants such as squalene epoxidase, sterol methyltransferase I, sterol C4-demethylase, obtusifoliol C14 α -demethylase, sterol C5-desaturase, and sterol methyl transferase II.

Example 3. Enhancement of phytosterol biosynthesis in seeds of *Arabidopsis* transgenic plants by constitutive expression of different forms of *Arabidopsis* and rubber HMGR enzymes.

Arabidopsis transgenic plants were generated using *Agrobacterium* mediated transformation of constructs

(pMON53733, pMON53734, pMON53735, pMON53736, pMON53737, pMON53738, pMON53739, pMON53740) carrying cDNA encoding different forms of *Arabidopsis* and rubber HMGR enzymes driven by CaMV enhanced 35S promoter (Figures 13-20). The transformed *Arabidopsis* seeds carrying each of the above constructs were selected on kanamycin (50µg/ml) medium to select for transformants expressing the selectable marker, the NPTII gene driven by CaMV 35S promoter. Kanamycin resistant *Arabidopsis* transgenic plants were grown in green house for maturity and seeds were collected from each of the transgenic lines for sterol analysis. About 50 mg of seeds from each transgenic line were weighed, homogenized and used for saponification to extract sterols as described in Example 2.

Figures 21-26 describe the sterol analysis data obtained from the transgenic lines carrying each of the above constructs. Figure 27 shows the effect on different sterol end products and pathway intermediate accumulation when different forms of rubber HMGR cDNAs were expressed constitutively in transgenic *Arabidopsis* plants. When truncated rubber HMGR (with or without linker region) was overexpressed the total sterol accumulation in seeds increased by 2.9 to 3.7-fold as compared with the wild type control plants. The sterol end products such as campesterol and sitosterol showed 1.5 to 2 -fold increase in the lines expressing truncated form of rubber HMGR (with and without linker). However the sitostanol end product accumulation in the transgenic lines harboring the truncated form of rubber HMGR (with and without linker) was enhanced by 2.8 to 7-fold. There is a significant accumulation of pathway intermediates such as cycloartenol and 24-methylene cycloartenol in the seeds of the transgenic lines transformed with the truncated form of rubber HMGR (with and

without linker region). The wild type control plants used in the experiment do not accumulate both of the pathway intermediates.

5 Example 4. Comparison of Steroid Compounds from HMGR Constructs in a Yeast HMGR1 Knockout Mutant

The effects on the sterol levels of the expression of various HMGR constructs expressed in a yeast HMGR1 knockout mutant were compared. Constructs containing a nucleic acid
10 encoding the full length HMGR polypeptides from *Arabidopsis* and rubber were compared to those encoding a truncated *Arabidopsis* or rubber HMGR polypeptide that were lacking both the membrane binding and linker region of HMGR. The control yeast cells were transformed with a similar
15 construct lacking a polypeptide encoding any form of HMGR.

Yeast cells transformed with *Arabidopsis* HMGR and rubber HMGR constructs accumulated approximately the same amounts of zymosterol and ergosterol, but more squalene than the control yeast.

20 Transformed yeast cells having rubber HMGR constructs accumulated about the same amount of ergosterol, but about twice as much squalene and zymosterol than the control yeast.

Transformed yeast cells having *Arabidopsis* tHMGR
25 constructs accumulated three times as much squalene, twice as much zymosterol, and about 30 percent more ergosterol than the control yeast.

Transformed yeast cells having rubber tHMGR constructs accumulated three times as much squalene, four times as much
30 zymosterol, and about 50 percent more ergosterol than the control yeast.

The data are shown in a Figure 28, "Plant HMGR1 Constructs in Yeast HMGR1 Knockout Mutant".

Example 5. Gene sequences for all genes listed in the application

The sequences obtained from the NCBI public database are SEQ ID NO.: 1,2,3,20,21,22,23. These sequences are
5 included in the appendix and denoted as follows:

Appendix A= SEQ ID NO. 1,
Appendix B= SEQ ID NO. 2,
Appendix C= SEQ ID NO. 3,
Appendix D= SEQ ID NO. 20,
10 Appendix E= SEQ ID NO. 21,
Appendix F= SEQ ID NO. 22,
Appendix G= SEQ ID NO. 23.

SEQ ID 1 = *Arabidopsis* squalene epoxidase protein
15 sequence (Accession NO: AC004786) **See Appendix A**

SEQ ID 2 = *Arabidopsis* squalene epoxidase (Accession
NO: N64916) **See Appendix B**

SEQ ID 3 = *Arabidopsis* squalene epoxidase (Accession
NO: T44667) **See Appendix C**

20 SEQ ID 4 = *Arabidopsis* squalene epoxidase (clone ID:
ATA506263) nucleotide sequence

GAATTCCCGGGTCGACCCACGCGTCCGCTTATAGATAAGGATATGGCCTTTACGA
25 ACGTTTGCCTATGGACGCTACTCGCCTTCATGCTGACTTGGACAGTGTTCTACGTCACAA
ACAGGGGGAAGAAGGCGACGCAGTTGGCGGATGCGGTGCTTGAAGAGCGAGAAGACGGTG
CTACTGACGTTATCATCGTTGGGGCTGGAGTAGGCGGCTCGGCTCTCGCATATGCTCTTG
CTAAGGACGGGCGTCGAGTCCATGTAATAGAGAGGGACCTGAGAGAACCAGAGAGAATCA
TGGGTGAGTTTATGCAACCAGGAGGACGACTCATGCTCTCTAAGCTTGGTCTTGAAGATT
30 GTTTGGAGGGAATAGATGCCCAAAAAGCCACGGGCATGACAGTTTATAAGGACGGAAAAG
AAGCAGTCGCATCTTTTCCCGTGGACAACAACAATTTTCCTTTTGATCCTTCGGCTCGAT
CTTTTCACAATGGCCGATTTCGTCCAACGATTGCGGCAAAAAGGCTTCTTCTCTTCCCAATG
TGCGCCTGGAAGAAGGAACGGTGAAGTCTTTGATAGAAGAAAAGGAGTGATCAAAGGAG
TGACATACAAAAATAGCGCAGGCGAAGAAACAACAGCCTTGGCACCTCTCACTGTAGTAT
35 GCGACGGTTGCTACTCAAACCTTCGCCGGTCTCTTAATGACAACAATGCGGAGGTTCTGT
CATACCAAGTTGGTTTTATCTCAAAGAACTGTCAGCTTGAAGAACCCGAAAAGTTAAAGT
TGATAATGTCTAAACCTCCTTCACCATGTTGTATCAAATCAGCAGCACCGACGTTCTGTT
GTGTTTTTGAAGTTCTCCCCAACACATTCCTTCTATTTCAAATGGTGAAATGGCTACTT
TCGTGAAGAACACTATTGCTCCTCAGGTACCTTTAAAACTCCGCAAAATATTTTTTGAAAG
40 GGATTGATGAAGGAGAACATATAAAAGCCATGCCAACAAAGAAGATGACAGCTACTTTGA
GCGAGAAGAAAGGAGTGATTTTATTGGGAGATGCATTCAACATGCGTCATCCAGCAATCG

CATCTGGAATGATGGTTTTATTATCTGACATTCTCATTTTTACGCCGTCTTCTCCAGCCAT
TAAGCAACCTTGGCAATGCGCAAAAAATCTCACAAGTTATCAAGTCCTTTTATGATATCC
GCAAGCCAATGTCAGCGACAGTTAACACGTTAGGAAATGCATTCTCTCAAGTGCTAGTTG
CATCGACGGACGAAGCAAAAGAGGCAATGAGACAAGGTTGCTATGATTACCTCTCTAGTG
5 GTGGGTTTCGCACGTCAGGGATGATGGCTTTGCTAGGCGGCATGAACCCTCGTCCGATCT
CTCTCATCTATCATCTATGTGCTATCACTCTATCCTCCATTGGCCATCTACTCTCTCCAT
TTCCCTCTCCCCTTGGCATTGTCATAGCCTTCGACTTTTTGGTTTGGCTATGAAAATGT
TGGTTCCCCATCTCAAGGCTGAAGGAGTTAGCCAAATGTTGTTTCCAGTCAACGCCGCCG
CGTATAGCAAAAGCTATATGGCTGCAACGGCTCTTTAAACACTGGTGCTTTAAACTGCA
10 AAATATAACACATATATAAATCCCGAATCTTTGTGATTCTGCATATATTGTGTTCTACAA
TTATTCTCATATAAATGAAAATTGTTCTACGTAAAAGTAAAAAGAAGGAATTGTAATACT
AATAAAACGAGTTTTTAATTCTGTTGAATGCTTGTGTATATTGGTGAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC

15 SEQ ID 5 = *Arabidopsis* squalene epoxidase (clone ID:
ATA506263) amino acid translation

EFPGRPTRPLIDKDMAFTNVCLWTL LAFMLTWTVFYVTNRGKKATQLADAVVEER
EDGATDVIIVGAGVGSALAYALAKDGRRVHVIERDLREPERIMGEFMOQPGRLMLSKLG
20 LEDCLEGIDAQKATGMTVYKDGKEAVASFPVDNNNFPDPSPARSFHNGRFVQRLRQKASS
LPNVRLEEGTVKSLIEEKGVIKGVITYKNSAGEETTALAPLTVVCDGCYSNLRRSLNDNNA
EVLSYQVGFI SKNCQLEPEKCLKLIMSKPSFTMLYQISSSTDVRCVFEVLPNNIPSISNGE
MATFVKNTIAPQVPLKLRKI FLKGIDEGEHIKAMPTKKMTATLSEKKGVILLGDAFNMRH
PAIASGMMVLLSDILILRRL LQPLSNL GNAQKISQVIKSFYDIRKPMSATVNTLGNAFSQ
25 VLVASTDEAKEAMRQGCYDYLSSGGFRTSGMMALLGGMNPRPISLIYHLCAITLSSIGHL
LSPFPSPLGIWHSRLRFLGLAMKMLVPHLKAEGVSQMLFPVNAAAYS KSYMAATAL*

30 SEQ ID 6 = *Arabidopsis* squalene epoxidase (clone ID:
ATA304243) nucleotide sequence

GAATTCCCGGGTCGACCCACGCGTCCGCGGACGCGTGCGGATTGAGAACAAATAGA
TTTGGTTATATATGGCTTTTACGCACGTTTGTTTATGGACGTTAGTCGCCTTCGTGCTGA
CGTGGACGGTGTTCTACCTTACCAACATGAAGAAGAAGGCGACGGATTTGGCTGATACGG
TGGCTGAGGATCAAAAAGACGGTGCTGCTGACGTCATTATCGTCGGGGCTGGTGTAGGTG
35 GTTCGGCTCTCGCATATGCTCTTGCTAAGGATGGGCGTCGAGTACATGTGATCGAGAGGG
ACATGAGAGAACCAGAAAGAAATGATGGGTGAGTTTATGCAACCTGGCGGACGACTCATGC
TTTCTAAACTTGGCCTTCAAGATTGCTTGGAAGACATAGATGCACAGAAAGCCACGGGTT
TGGCAGTTTATAAAGATGGAAAAGAAGCAGACGCACCTTTTCCAGTGGATAACAACAATT
TTTCTTATGAACCTTCTGCTCGATCTTTT CACAATGGCCGATTCTGTTCAACAACCTGCGTC
40 GAAAGGCTTTTTCTCTTTCCAATGTGCGCCTGGAAGAAGGAACGGTGAAGTCTTTACTAG
AAGAAAAAGGAGTGGTCAAAGGAGTGACATACAAGAATAAAGAAGGCGAAGAAACAACAG
CCTTGGCACCTCTCACTGTGGTATGCGACGGTTGCTACTCAAACCTTCGTGCGGTCTCTTA
ATGATGACAACAATGCTGAGATTATGTCGTACATAGTTGGTTACATCTCAAAGAATTGTC
GGCTTGAAGAACCCGAAAAGCTACACTTGATATTGTCTAAACCATCTTTACCATGGTAT
45 ACCAAATAAGCAGCACTGACGTTTCGTTGTGGTTTTGAGGTTCTCCCCGAAAATTTTCCTT
CTATTGCAAATGGTGAAATGTCTACTTT CATGAAGAATACTATAGTTCTCAGGTACCTC
CAAACTCCGCAAAATATTTTTGAAAGGTATAGATGAGGGAGCACACATAAAAGTGGTGC
CGGCAAAGCGCATGACATCTACTTTAAGCAAGAAGAAAGGTGTGATTGTATTGGGAGATG
CATTCAATATGCGTCATCCAGTTGTTGCATCTGGAATGATGGTTTTACTGTGCGGACATTC
50 TCATTCTACGCCGTCTTCTTCAGCCATTAAGCAACCTCGGCGATGCAAACAAAGTCTCAG
AAGTTATCAATTCCTTTTATGATATCCGCAAGCCAATGTCGGCGACGGTTAACACATTGG

132

GAAATGCATTTTCTCAAGTACTAATTGGATCAACGGATGAAGCAAAGAGGCAATGAGAC
AGGGTGTCTATGATTACCTTTGTAGTGGCGGGTTTCGTACGTCAGGGATGATGGCTCTGC
TCGGCGGCATGAATCCTCGTCCTCTCTCTCTCGTCTATCATCTTTGTGCCATCACTCTAT
CCTCCATTGGCCAACTGCTCTCTCCATTTCCTCTCCCCCTTCGCATTTGGCATAGCCTCA
5 AGCTTTTTTGGTTTGGCCATGAAAATGTTGGTTCCCAATCTCAAAGCTGAAGGAGTTAGCC
AAATGTTGTTTCCAGCAAATGCAGCCGCGTATCACAAAAGCTATATGGCTGCAACCACTC
TCTAAACTTTGATGCTCTCAATCGCAATATATATGGAGCACGAATCTATGTGATTGTGCA
TTTGGTAAACGTGTATTGCAGTGCTTATAATTATTAGTATGTAACGGGGAAAAGTTCTAA
ACACAAAAAATAAACTTTTGAATGTTATATGTGTGAATTATTTTTGTTGTTACAAGTAA
10 TGCTCTTTTTTTTTTAGCTTCACACATGTATTATTGGAGCTAATTTTTTGTCTCTGTTC
TTTTATTTTTGTTTTCTTACTGTATTTACTTTGAAAAGTTTCGTTTTTATACATATTGGAC
ATTTTTTAAA
AAAGGGCGGC
CGC

15

SEQ ID 7 = *Arabidopsis* squalene epoxidase (clone ID:
ATA304243) amino acid translation

MAFTHVCLWTLVAFVLTWTVFYLTNMKKKATDLADTVAEDQKDGAADVIIIVGAGVGGG
20 AYALAKDGRRVHVIERDMREPERMMGEFMQPGRLMLSKLGLQDCLEDIDAQKATGLAVY
KDGKEADAPFPVDNNNFSYEPSARSFHNGRFVQQLRRKAFSLSNVRLEEGTVKSLLEEK
VVKGVITYKNKEGEETTALAPLTVVCDGCYSNLRSLNDDNNAEIMSYIVGYISKNCRL
PEKLHLILSKPSFTMVYQISSTDVRCGFVLPENFPSIANGEMSTFMKNTIVPQVPPKLR
KIFLKGIDEGAHIKVVPKRMSTLSKKKGVIIVLGDFAFNMRHPVVASGMMVLLSDILIL
25 RLLQPLSNLGDANKVSEVINSFYDIRKPMSATVNTLGNAFSQVLIGSTDEAKEAMRQGVY
DYLCSSGGFRTSGMMALLGGMNRPPLSLVYHLCAITLSSIGQLLSPFPSPLRIWHSCLKLFG
LAMKMLVPNLKAEGVSQ MLFPANAAAYHKSYMAATTL*

30 SEQ ID 8 = *Arabidopsis* squalene epoxidase (clone ID:
ATA102071) nucleotide sequence

AAATCATATTGAGAACAAATAGATTGGTTATATATGGCTTTTACGCACGTTTGT
TTATGGACGTTAGTCGCCTTCGTGCTGACGTGGACGGTGTCTACCTTACCAACATGAAG
AAGAAGGCGACGGATTTCGGCTGATACGGTGGCTGAGGATCAAAAAGACGGTGCTGCTGAC
35 GTCATTATCGTCGGGGCTGGTGTAGGTGGTTCGGCTCTCGCATATGCTCTGCTAAGTGTG
CGCCTGGAAGAAGGAACGGTGAAGTCTTTACTAGAAGAAAAGGAGTGGTCAAAGGAGTG
ACATACAAGAATAAAGAAATGCGAACAAACAACAGCCTTGGCACCTCTCACTGTGGTATGC
GACGGTTGCTAATCAAACCTTCGTGGTCTCTTAATG

40 SEQ ID 9 = *Arabidopsis* squalene epoxidase (clone ID:
ATA102071) amino acid translation

MAFTHVCLWTLVAFVLTWTVFYLTNMKKKATDLADTVAEDQKDGAADVIIIVGAGV
GGGALAYALLSVRLEEGTVKSLLEEKGVVKGVITYKNKECEQTALAPLTVVCDGC
45

SEQ ID 10 = *Arabidopsis* squalene epoxidase (clone ID:
ATA504158) nucleotide sequence

50 CACAAAGCAAAAAAATCTCTGTAAAAGCAGAACGATAATGGAGTCACAATTATGG
AATTGGATCTTACCTCTTTTGATCTCTTCTCTCCTCATCTCCTTCGTGCTTTCTATGGA

TTCTTCGTCAAACCGAAGCGGAACGGTCTCCGTCACGATCGGAAAAC TGTTCCTACCGTC
ACCTCCGACGTCGGATCTGTTAATATTACCGGAGATACTGTCGCTGATGTCATTGTTGTT
GGAGCTGGTGTGCTGGTCTGCTCTTGCTTATACTCTTGGAAGGGGAAATTTAAACGC
CGAGTTCATGTGATTGAAAGAGATTTATCGGAGCCTGATCGTATTGTTGGGGAGTTGTTA
5 CAGCCTGNNGGTTACCTCAAGTTACTGGAGTGTGGAATTGGAGATTGTGTGGAAGAAATA
GATGCTCAGCNTGTGTATGGTTATGCACTTTTTTAAAAATGGG

SEQ ID 11 = *Arabidopsis* squalene epoxidase (clone ID:
ATA504158) amino acid translation

10 TKQKNLCKSRTIMESQLWNWILPLLISLLISFVAFYGGFFVKPKRNLRLHDKTV
STVTSDVGSVNITGDTVADVIVVGAGVAGSALAYTLGKGKFKRRVHVIERDLSEPDRIVG
ELLQPXGYLKLLECGIGDCVEEIDAQXVYGYALFKNG

15 SEQ ID 12 = *Arabidopsis* obtusifoliol C14 α -demethylase
nucleotide sequence (Accession NO: complement, join
AC002329:37461...38456, AC002329:39121...39546) (homolog of
sorghum obtusifoliol C14 α -demethylase) nucleotide sequence

20 CGTGTTTTACAAATTTCTTTGTTGGTTTTCCACAGATTTAAAGAACCCTAACGA
GAGAAAAAATGGACTGGGATTACTATACGCTGTTGAAGACGAGTGTGGCTATTATTATA
GTGTTTGTGTGGCCAACTCATAACCTCCTCCAAATCCAAGAAGAAAACAAGTGTGCTC
CCACTCCCTCCAGTTCTTCAAGCGTGGCCTCCATTTATCGGATCCCTAATCCGCTTCATG
AAAGGTCCAATAGTGCTACTTAGAGAGGAATATCCTAAGCTTGGAAAGTGTTCACAGTG
25 AAGCTTCTTCACAAAACATCACTTTTCTCATCGGTCCCGAAGTCTCGTCCCACTTTTTC
AACGCTTATGAATCTGAAGTCAAGCAGCCAGAAAGAAATTTACAAATTTAATGTGCCTACTTTT
GGCCCCGGAGTTGTGTTTGATGTTGACTATCCCGTTTCGGATGGAGCAGTTCCGATTCTTC
TCCAGCGCTCTCAAGGATTACTTCTCAAAATGGGGAGAAAGTGGGGAAGTGGATCTAAAG
GCCGAGTTAGAGCGTCTAATCACCTTGACTGCTAGTAGATGTCTATTGGGTGCGAGAAGTC
30 CGTGACCAACTTTTTGATGATGTTGCTCCATTGTTCCATGACCTTGATAAAGGCATGCAA
CCCATAAGTGTATCTTCCCAAAGCTCCCCATTCCAGCTCACAATTGTCGTGACCGTGCT
CGCGGAAAGATTGCAAAAATCTTTTCAAACATCATAGCAACAAGAAAACGCTCTGGTGAC
AAATCAGAGAACGACATGCTACAATGTTTCATCGACTCAAAGTACAAAGACGGTAGAGAG
ACAACTGAATCTGAAGTAACTGGTTTGCTCATTGCTGGTTTGTTCAGGACAACATACA
35 AGCTCTATCACTGCCACATGGACCGGTGCTTATCTAATTCAAACAAACACTGGTGGTCC
GCGGCTTTGGACGAGCAGAAGAACTGATTGGAAAACATGGGGACAAGATCGACTACGAT
GTTTTGTCTGAGATGGATTTTCTGTTTCGCAGTGCAAAAGAAGCTTTAAGGCTTCACCT
CCAAAGATCTTACTGCTGAGAACAGTACACAGTGATTTACCGTGACAACCTCGAGAAGGA
AAGCAATATGAGATACCAAAGGGTCATATCGTTGCAACTTCTCCTGCATTCGCCAACCGC
40 TTACCTCATGTCTACAAAGATCCGGAAAATTTTGATCCGGATAGATTTTCAAAGGAAAGA
GAAGAGGATAAAGCAGCTGGTTCGTGTTTCATACATCTTTTGGGAGCTGGTAGGCACGAG
TGTCTGGTGGATCATTTGCGTTCTTGCAGATCAAAGCCGTATGGTGTCACTTATTGAGA
AACTTTGAGCTTGAGTTAGTGTACCTTTCCCTGAAATCAACTGGAATGCTTTGGTCGTT
GGTGCTAAAGGAAATGTCATGGTTCGTTACAAGCGTCGTCCCTTTTCTTAA
45

SEQ ID 13 = *Arabidopsis* obtusifoliol C14 α -demethylase
nucleotide sequence (Accession NO: complement, join

AC002329:37461...38456, AC002329:39121...39546) (homolog of sorghum obtusifoliol C14 α -demethylase) amino acid translation

5 MDWDYYTLLKTSVAIIIVFVVAKLITSSKSKKKTSVVPLPPVLQAWPPFFIGSLIR
FMKGPIVLLREEYPKLGSVFTVKLLHKNITFLIGPEVSSHFFNAYESELQKEIYKFNPV
TFGPGVVFDVDYDYPVRMEQFRFFSSALKDYFSKWGESGEVDLKAELERLITLTASRCLLGR
EVRDQLFDDVAPLFHDLDKGMQPISVIFPKLPIPAHNCRDRARGKIAKIFSNI IATRKRS
GDKSENDMLQCFIDSKYKDGRETTESEVTGLLIAGLFAGQHTSSITATWTGAYLIQNKHW
10 WSAALDEQKKLIGKHGDKIDYDVLSEMDFLFRSAKEALRLHPPKILLRLTVHSDFTVTTR
EGKQYEIPKGHIVATSPAFANRLPHVYKDPENFDPDRFSKEREEDKAAGSCSYISLGAGR
HECPGGSFAFLQIKAVWCHLLRNFELELVSPFPEINWNALVVGAKGNVMVRYKRRPFS*

SEQ ID 14 = *Arabidopsis* obtusifoliol C14 α -
15 demethylase(clone ID: ATA101105) nucleotide sequence

GACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCTG
GCTCGAGCTTGTTCACAAAAAGATTACTTTTCTTATTGGTCCTGAAGTCTCTGCTCATT
TTTCAAAGCTTCTGAATCTGATCTTAGTCAGCAGGAAGTGTATCAGTTCAATGTCCTTAC
20 TTTTGGTCCTGGAGTTGTTTTCGATGTTGATTATTCTGTTTCGTCAGGAGCAGTTCCGTT
CTTCACTGAGGCACCTTAGAGTTAACAAGTTGAAGGGTTATGTGGATATGATGGTTACTGA
AGCTGAGGATTACTTCTCTAAATGGGGAGAGAGTGGTGAAGTTGATATTAAGGTTGAGCT
AGAGAGGCTCATCATCTTGACTGCAAGTGATGTTTACTGGGTCGAGAAGTTCGTGATCAG
CTTTTTGATGATGTCTCTGCTTTGTTCCATGACCTTGACAATGGAATGCTTCCCATCAGT
25 GCTTCCCATCAGTGTTCTCTTCCCATATCTCCCAATTCCAGCTCACCG

SEQ ID 15 = *Arabidopsis* obtusifoliol C14 α -
demethylase(clone ID: ATA101105) amino acid translation

30 HYRRAMTSHARVRKLGIRLELVHKKITFLIGPEVSAHFFKASESDLSQQEVYQFN
VPTFGPGVVFDVDYSVRQEQQFGSSLRHLELTS

SEQ ID 16 = *Arabidopsis* obtusifoliol C14 α -
demethylase(clone ID: ATA202967) nucleotide sequence

35 TCGACCCCGCGTCCGCGGACGCGTGGGATCAGCTTCAAGCTTAAGAGAGCTTCGA
AAGCGAAAGCGACGATTTCTTCTCCATCGTGAGAGCAAATCTCCAGAGCCGTTTTCTCTT
CTTCTTCTTCTCCTCGCGCCGTCTCTGAACTCCATCATCGTATCAATCAAATTGCTTC
CTCCTCCAAATTGAAAAACAATGGAATTGGATTCCGAGAACAAATTGTTGAAGACGGGTT
40 TGGTTATAGTGGCGACACTTGTTATAGCCAACTCATCTTCTCTTCTTCACTTCTGATT
CTAAGAAGAAGCGTCTTCTCCTACTCTTAAAGCTTGGCCTCCATTGGTTGGAAGTCTTA
TCAAATTCTTGAAAGGACCTATTATTATGCTTAGAGAGGAATACCCTAAGCTTGGAAAGTG
TGTTTACTGTTAATCTTGTTACAAAAAGATTACTTTTCTTATTGGTCCTGAAGTCTCTG
CTCATTTTTTTCAAAGCTTCTGAATCTGATCTTAGTCAGCAGGAAGTGTATCAGTTCAATG
45 TCCCTACTTTTGGTCCTGGAGTTGTTTTCGATGTTGATTATTCTGTTCGTGAGGAGCAGT
TTCGGTTCTTCACTGAGGCACTTAGAGTTAACAAGTTGAAGGGTTATGTGGATATGATGG
TACTGAAGCTGAGGATTACTTCTCTAAATGGGGAGAGAGTGGTGAAGTTGATATTAAGG
TTGAGCTAGAGAGGCTCATCATCTTGACTGCAAGTAGATGTTTACTGGGTCGAGAAGTTC
GTGATCAGCTTTTTGATGATGTCTCTGCTTTGTTCCATGACCTTGACAATGGAATGCTTC
50 CCATCAGTGTTCTCTTCCCATATCTCCCAATTCCAGCTCACCGCCGTCGTGACCGTGCCC

GAGAAAAGCTTTCGGAGATTTTCGCAAAAATCATTGGGTCGAGAAAACGCTCTGGAAAAA
CAGAGAACGACATGCTGCAGTGTTTCATCGAATCAAAGTACAAAGATGGTAGACAGACAA
CCGAATCTGAAGTCACTGGTTTGCTCATTGCTGCTCTGTTGTCAGGACAACACACGAGCT
CTATCACTTCCACCTGGACCGGTGCTTATCTGATGCGATACAAAGAGTACTTCTCAGCTG
5 CTCTTGATGAGCAGAAGAACCTGATTGCGAAACATGGAGACAAGATCGATCATGATATCT
TATCCGAGATGGATGTTTCTCTACCGCTGCATTAAGGAAGCGTTGAGGCTTCACCCTCCAC
TCATCATGTTAATGAGAGCCTCGCACAGTGATTTTCAGCGTGACAGCTCGGGATGGAAAAA
CTTACGATATCCCAAAGGGTCACATCGTTGCAACCTCCCCTGCATTTGCCAACCGCTTAC
CGCACATCTTCAAAGACCCCGACACCTACGACCCAGAAAGATTCTCCCCTGGAAGAGAAG
10 AGGACAAAGCCGCGAGGGGCATTCTCGTACATTGCATTTCGGAGGGGGGAAGGCACGGGTGCC
TTGGAGAGCCGTTTGCTTACCTGCAGATCAAAGCCATATGGAGTCATTTGTTGAGGAAGT
TCGAGCTTGAGCTAGTTTTCACCGTTCCCTGAGATTGACTGGAACGCTATGGTGTTGGAG
TTAAAGCAATGTGATGGTGCCTTACAAGAGGCgCAGCTTCTTAAAGACAAGTTTAAG
GTTATTGCAGCTTTGGATTTTTCTCTCTGGTTTCTGCTTTTGTCCCTCTCTGGTT
15 TTAGTTTTGTTGTTGAATAATTCTTCTGTTTTTATAAACTGTTGTTACTCTTTAATTGAC
ATTTATTTTTAAGCTTCCTAAGTTTGTGGTTCAAAAAAAAAAAAAAGGCGGCGTTACT

SEQ ID 17 = *Arabidopsis obtusifoliol* C14 α -
demethylase(clone ID: ATA202967) amino acid translation

20 MELDSENKLLKTGLVIVATLVIKLIFFSFFTSDSKKKRLPPTLKAWPPLVGSLLIKFLKGP
IIMLREEYPKLGSVFTVNLVHKKITFLIGPEVSAHFFKASESDL SQQEVYQFNVPTFGPG
VVFVDVYSVRQEQFRFFTEALRVNKLKGYVDMMVTEAEDYFSKWGESGEVDIKVELERLI
ILTASRCLLGREVRDQLFDDVSALFHDLDNGMLPI SVLFYPYLP I PAHRRRDRAREKLSEI
25 FAKIIGSRKRSKGTENDMLQCFIESKYKDGRQTTESEVTGLLIAALFAGQHTSSITSTWT
GAYLMRYKEYFSAALDEQKNLIAKHGDKIDHDILSEMDVLYRCIKEALRLHPPLIMLMRA
SHSDFSVTARDGKTYDIPKGHIVATSPAFANRLPHIFKDPDTPYDPERFSPGREEDKAAGA
FSYIAFGGGRHGCLGEPFAYLQIKAIWSHLLRNFELELVSPFPEIDWNAMVVGKGNVMV
RYKRRQLS*

30 SEQ ID 18 = *Arabidopsis obtusifoliol* C14 α -
demethylase(clone ID: ATA403931) nucleotide sequence

TCGACCCCGCGTCCGCGGACGCGTGGGATCAGCTTCAAGCTTAAGAGAGCTTCGA
35 AAGCGAAAGCGACGATTTCTTCTCCATCGTGAGAGCAAATCTCCAGAGCCGTTTTCTCTT
CTTCTTCTTCTCCTCGCGCCGTCTCTGAAACTCCATCATCGTATCAATCAAATTGCTTC
CTCCTCAAATTGAAAAACAATGGAATTGGATTGCGAGAACAAATTGTTGAAGACGGGTT
TGGTTATAGTGGCGACACTTGTTATAGCCAAACTCATCTTCTCTTCTTCACTTCTGATT
CTAAGAAGAAGCGTCTTCTCCTACTCTTAAAGCTTGGCCTCCATTGGTTGGAAGTCTTA
40 TCAAATTCTTGAAAGGACCTATTATTATGCTTAGAGAGGAATACCCTAAGCTTGGAAGTG
TGTTTACTGTTAATCTTGTTTCAAAAAAGATTACTTTTCTTATTGGTCTGAAGTCTCTG
CTCATTTTTTCAAAGCTTCTGAATCTGATCTTAGTCAGCAGGAAGTGTATCAGTTCAATG
TCCCTACTTTTGGTCTGAGTTGTTTTCGATGTTGATTATTCTGTTTCGTCAGGAGCAGT
TTCGGTTCTTCACTGAGGCACTTAGAGTTAAACAAGTTGAAGGGTTATGTGGATATGATGG
45 TTAAGTGAAGCTGAGGATTACTTCTCTAAATGGGGAGAGAGTGGTGAAGTTGATATTAAGG
TTGAGCTAGAGAGGCTCATCATCTTGAAGTGAAGTAGATGTTTACTGGGTCGAGAAGTTC
GTGATCAGCTTTTTGATGATGTCTCTGCTTTGTTCCATGACCTTGACAATGGAATGCTTC
CCATCAGTGTTCTCTTCCCATATCTCCAATTCCAGCTCACCGCCGTCGTGACCGTGCCC
GAGAAAAGCTTTCGGAGATTTTCGCAAAAATCATTGGGTCGAGAAAACGCTCTGGAAAAA
50 CAGAGAACGACATGCTGCAGTGTTTCATCGAATCAAAGTACAAAGATGGTAGACAGACAA

CCGAATCTGAAGTCACTGGTTTGCTCATTGCTGCTCTGTtTGCAGGACAACACACGAGCT
 CTATCACTTCCACCTGGACCGGTGCTTATCTGATGCGATACAAAGAGTACTTCTCAGCTG
 CTCTTGATGAGCAGAAGAACCTGATTGCGAAACATGGAGACAAGATCGATCATGATATCT
 TATCCGAGATGGATGTTCTCTACCGCTGCATTAAGGAAGCGTTGAGGCTTCACCCTCCAC
 5 TCATCATGTTAATGAGAGCCTCGCACAGTGATTTTCAGCGTGACAGCTCGGGATGGAAAAA
 CTTACGATATCCCAAAGGGTCACATCGTTGCAACCTCCCCTGCATTTGCCAACCGCTTAC
 CGCACATCTTCAAAGACCCCGACACCTACGACCCAGAAAGATTCTCCCCTGGAAGAGAAG
 AGGACAAAGCCGCGAGGGGCATTCTCGTACATTGCATTCGGAGGGGGAAGGCACGGGTGCC
 TTGGAGAGCCGTTTGCTTACCTGCAGATCAAAGCCATATGGAGTCATTTGTTGAGGAACT
 10 TCGAGCTTGAGCTAGTTTCACCGTTCCCTGAGATTGACTGGAACGCTATGGTGGTTGGAG
 TTAAAGGCAATGTGATGGTGCGTTACAAGAGGCgcCAGCTTTCTTAAAGACAAGTTTAAG
 GTTATTGCAGCTTTGGATTTTCTCTCTGGTTTCTGCTTTGCTTTTGTCCCTCTCTGGTT
 TTAGTTTTGTTGTTGAATAATTCTTCTGTTTTTATAAACTGTTGTTACTCTTTAATTGAC
 ATTTATTTTTTAAGCTTCCTAAGTTTGTGGTTCAAAAAAAAAAAAAAGGCGGCGTTACT

15

SEQ ID 19 = *Arabidopsis* obtusifoliol C14 α -
 demethylase(clone ID: ATA403931) amino acid translation

MELDSENKLLKTGLVIVATLVI AKLIFSFFTSDSKKRLPPTLKAWPPLVGSLIKFLKGP
 20 IIMLREEYPKLGSVFTVNLVHKKITFLIGPEVSAHFFKASESDLSQQEVYQFNVPFTGPG
 VVFDVDYSVRQEQFRFFTEALRVNKLKGYVDMMVTEAEDYFSKWGESGEVDIKVELERLI
 ILTASRCLLGREVRDQLFDDVSALFHDLDNGMLPISVLFPPYLP I PAHRRRDRAREKLSEI
 FAKIIGSRKRSGKTENDMLQCFIESKYKDGRQTTESEVTGLLIAALFAGQHTSSITSTWT
 GAYLMRYKEYFSAALDEQKNLIAKHGDKIDHDILSEMDVLYRCIKEALRLHPPLIMLMRA
 25 SHSDFSVTARDGKTYDIPKGHIVATSPAFANRLPHIFKDPD TYDPERFSPGREEDKAAGA
 FSYIAFGGGRHGCLGEPFAYLQIKAIWSHLLRNFELELVSPFPEIDWNAMVVGKGNVMV
 RYKRRQLS*

SEQ ID 20 = *Arabidopsis* sterol methyl transferase I
 30 protein sequence (Accession NO: U71400) See Appendix D

SEQ ID 21 = Tobacco sterol methyl transferase I protein
 sequence (from Prof. Pierre Benveniste Accession NO: U81312)
 See Appendix E

35

SEQ ID 22 = *Arabidopsis* sterol methyl transferase II
 protein sequence (Accession NO: X89867) (from Prof. Pierre
 Benveniste) See Appendix F

SEQ ID 23 = *Arabidopsis* sterol C5-desaturase protein
 40 sequence (Accession NO: X90454) See Appendix G

SEQ ID 24 = Rubber truncated HMGR1m1 (S566 to A)
 nucleotide sequence

ATGGCACGCGCCTCCCATGACGTGTGGGACCTCGAAGATACGGATCCCAACTACCTCATC
 45 GATGAAGATCACCGTCTCGTTACTTGCCCTCCCGCTAATATATCTACTAAGACTACCAT
 ATTGCCGCACCTACCAAATTGCCTACCTCGGAACCCTTAATTGCACCCTTAGTCTCGGAG
 GAAGACGAAATGATCGTCAACTCCGTCGTGGATGGGAAGATACCCTCCTATTCTCTGGAG
 TCGAAGCTCGGGGACTGCAAACGAGCGGCTGCGATTGACGCGAGGCTTTGCAGAGGATG
 50 ACAAGGAGGTGCGCTGGAAGGCTTGCCAGTAGAAGGGTTCGATTACGAGTCGATTTTAGGA

CAATGCTGTGAAATGCCAGTGGGATACGTGCAGATTCCGGTGGGGATTGCGGGGCCGTTG
 TTGCTGAACGGGCGGGAGTACTCTGTTCCAATGGCGACCACGGAGGGTTGTTTGGTGGCG
 AGCACTAATAGAGGGTGTAAGGCGATTACTTGTGAGGTGGGGCCACCAGCGTCTTGTTG
 AAGGATGGCATGACAAGAGCGCCTGTTGTAAGATTTCGCGTCGGCGACTAGAGCCGCGGAG
 5 TTGAAGTTCTTCTTGGAGGATCCTGACAATTTTGATACCTTGGCCGTAGTTTTTAACAAG
 TCCAGTAGATTTGCGAGGCTCCAAGGCATTAAATGCTCAATTGCTGGTAAGAATCTTTAT
 ATAAGATTGAGCTGCAGCACTGGCGATGCAATGGGGATGAACATGGTTTCTAAAGGGGTT
 CAAAACGTTCTTGAATTTCTTCAAAGTGATTTTTCTGATATGGATGTCATTGGAATCTCA
 GGAAATTTTTGTTTCGGATAAGAAGCCTGCTGCTGTAAATTGGATTGAAGGACGTGGCAAA
 10 TCAGTTGTTTGTGAGGCAATTATCAAGGAAGAGGTGGTGAAGAAGGTGTTGAAAACCAAT
 GTGGCCTCCCTAGTGGAGCTTAACATGCTCAAGAATCTTGCTGGTTCTGCTGTTGCTGGT
 GCTTTGGGTGGATTTAATGCCCATGCAGGCAACATCGTATCTGCAATCTTTATTGCCACT
 GGCCAGGATCCAGCACAGAATGTTGAGAGTTCTCATTGCATTACCATGATGGAAGCTGTC
 AATGATGGAAGGATCTCCATATCTCTGTGACCATGCCCTCCATTGAGGTGGGTACAGTC
 15 GGAGGTGGAACCTCAACTTGCATCTCAGTCTGCTTGTCTCAATTTGCTTGGGGTGAAGGGT
 GCAAACAAAGAGTCGCCAGGATCAAACCTCAAGGCTCCTTGCTGCCATCGTAGCTGGTTCA
 GTTTTGGCTGGTGAGCTCTCCTTGATGTCTGCCATTGCAGCTGGGCAGCTTGTCAAGAGT
 CACATGAAGTACAACAGAGCCAGCAAAGATATGTCTAAAGCTGCATCTTAG

20 SEQ ID 25 = Rubber truncated HMGR1m1 (S566 to A) amino
 acid translation
 MARASHDVWDLEDTPNYLIDEDHRLVTCPPANISTKTTIIAAPTKLPTSEPLIAPLVSE
 EDEMIVNSVVDGKIPSYSLESKLGDCKRAAIRREALQRMTRRSLEGLPVEGFDYESILG
 QCCEMPVGYVQIPVGIAGPLLLNGREYSVPMATTEGCLVASTNRGCKAIYLSGGATSVLL
 25 KDGMTTRAPVVRFASATRAAELKFFLEDPDNFDTLAVVFNKSSRFARLQGIKCSIAGKNLY
 IRFSCSTGDAMGMNMVSKGVQNVLEFLQSDFSMDVIGISGNFCSDDKPAAVNWIEGRGK
 SVVCEAI IKEEVVKKVLKTNVASLVELNMLKNLAGSAVAGALGGFNAHAGNIVSAIFIAT
 GQDPAQNVESSHCI TMMEAVNDGKDLHISVTMPSIEVGTGVTGGGTQLASQSACLNLLGVKG
 ANKESPGSNSRLLAAIVAGSVLAGELSLMSAIAAGQLVKSHMKYNRASKDMSKAAS

30

SEQ ID. 26 = Rubber truncated HMGR1m2 (S567 to A)
 nucleotide sequence
 35 ATGGCACGCGCCTCCCATGACGTGTGGGACCTCGAAGATACGGATCCCAACTACCTCATC
 GATGAAGATCACCGTCTCGTTACTTGCCCTCCCGCTAATATATCTACTAAGACTACCATT
 ATTGCCGCACCTACCAAATTGCCTACCTCGGAACCCTTAATTGCACCCTTAGTCTCGGAG
 GAAGACGAAATGATCGTCAACTCCGTCGTGGATGGGAAGATACCCTCCTATTCTCTGGAG
 TCGAAGCTCGGGGACTGCAAACGAGCGGCTGCGATTTCGACGCGAGGCTTTGCAGAGGATG
 40 ACAAGGAGGTCGCTGGAAGGCTTGCCAGTAGAAGGGTTCGATTACGAGTCGATTTTAGGA
 CAATGCTGTGAAATGCCAGTGGGATACGTGCAGATTCCGGTGGGGATTGCGGGGCCGTTG
 TTGCTGAACGGGCGGGAGTACTCTGTTCCAATGGCGACCACGGAGGGTTGTTTGGTGGCG
 AGCACTAATAGAGGGTGTAAGGCGATTACTTGTGAGGTGGGGCCACCAGCGTCTTGTTG
 AAGGATGGCATGACAAGAGCGCCTGTTGTAAGATTTCGCGTCGGCGACTAGAGCCGCGGAG
 45 TTGAAGTTCTTCTTGGAGGATCCTGACAATTTTGATACCTTGGCCGTAGTTTTTAACAAG
 TCCAGTAGATTTGCGAGGCTCCAAGGCATTAAATGCTCAATTGCTGGTAAGAATCTTTAT
 ATAAGATTGAGCTGCAGCACTGGCGATGCAATGGGGATGAACATGGTTTCTAAAGGGGTT
 CAAAACGTTCTTGAATTTCTTCAAAGTGATTTTTCTGATATGGATGTCATTGGAATCTCA
 GGAAATTTTTGTTTCGGATAAGAAGCCTGCTGCTGTAAATTGGATTGAAGGACGTGGCAAA
 50 TCAGTTGTTTGTGAGGCAATTATCAAGGAAGAGGTGGTGAAGAAGGTGTTGAAAACCAAT
 GTGGCCTCCCTAGTGGAGCTTAACATGCTCAAGAATCTTGCTGGTTCTGCTGTTGCTGGT

GCTTTGGGTGGATTTAATGCCCATGCAGGCAACATCGTATCTGCAATCTTTATTGCCACT
 GGCCAGGATCCAGCACAGAATGTTGAGAGTTCTCATTGCATTACCATGATGGAAGCTGTC
 AATGATGGAAAGGATCTCCATATCTCTGTGACCATGCCCTCCATTGAGGTGGGTACAGTC
 GGAGGTGGAAC TCAACTTGCATCTCAGTCTGCTTGTCTCAATTTGCTTGGGGTGAAGGGT
 5 GCAAACAAAGAGTCGCCAGGATCAAAC TCAAGGCTCCTTGCTGCCATCGTAGCTGGTTCA
 GTTTTGGCTGGTGAGCTCTCCTTGATGTCTGCCATTGCAGCTGGGCAGCTTGTCAAGAGT
 CACATGAAGTACAACAGATCCGCCAAAGATATGTCTAAAGCTGCATCTTAG

10 SEQ ID 27 = Rubber truncated HMGR1m2 (S567 to A) amino
 acid translation
 MARASHDVWDLED TDPNYLIDEDHRLVTCPPANISTKTTIIAAPT KLPTSEPLIAPLVSE
 EDEMIVNSVVDGKIPSY SLES KLGDCKRAAAIRREALQRMTRRSLEGLPVEGFDYESILG
 QCCEMPVGYVQIPVGIAGPLLLNGREYSVPMATTEGCLVASTNRGCKAIYLSGGATSVLL
 15 KDG MTRAPVVRFASATRAAELKFFLED PDNFDTLAVVFNKSSRFARLQGIKCSIAGKNLY
 IRFSCSTGDAMGMNMVSKGVQNVLEFLQSD FSDMDVIGISGNFCSDDKKPAAVNWIEGRGK
 SVVCEAI I KEEVVKKVLKTNVASLVELNMLKNLAGSAVAGALGGFNAHAGNIVSAIFIAT
 GQDPAQNVESSH C ITMMEAVNDGKDLHISVTMP SIEVGT VGGGTQLASQSACL NLLGVKG
 ANKESPGSNSRL LAIVAGSVLAGELSLMSAIAAGQLVKSHMKYNRS AKDMSKAAS

20

Example 6. *Arabidopsis* obtusifoliol C14 α -demethylase
 constructs

The *Arabidopsis* obtusifoliol C14 α -demethylase gene was
 amplified from two separate *Arabidopsis* mRNA samples (SIN 2
 25 and Keto-10) through use of primers BXK33 and BXK34, as
 described below.

BXK33 (SEQ ID 28): 5'-GAGATCTGAACCCTAACGAGAG-3'

30 BXK34 (SEQ ID 29): 5'-GGAGCTCTTAAGAAAAGGGACGACGC-3'

The primer BXK33 has a Bgl II cleavage site shown in
 bold. The primer BXK34 has a Sac I cleavage site shown in
 bold. The actual size of the structural gene is 1.445 Kb.

35 The *Arabidopsis* mRNA was amplified using a Perkin Elmer
 GeneAmp RT-PCR kit. The reverse transcription reaction used
 25 mM MgCl₂ (4 μ l; 5 mM final), 10X PCR buffer (2 μ l), di
 DEPC water (1 μ l), 2 μ l each of 1 mM solution of each of
 four dNTPs (dGTP, dATP, dUTP, dCTP), RNase inhibitor (1 μ l
 40 of 10 units per μ l stock), MMLV reverse transcriptase (1 μ l

of a 2.5 U/ μ l stock), Oligo d(T)16 Primer (1 μ l of a 2.5 μ M stock), and 2 μ l of an *Arabidopsis* polyA RNA sample. The reaction mix was incubated at room temperature (about 20°C) for 10 minutes, then in a PCR machine for one cycle (15 min. at 42°C, 5 min. at 99°C and 5 min. at 4°C).

Separate primer-mediated amplification reactions were carried out using Taq DNA polymerase and Vent DNA polymerase to obtain *Arabidopsis obtusifoliol* C14 α -demethylase cDNA from the amplified mRNA sample.

10

Taq PCR Reaction	Vent PCR Reaction
4 μ l 25 mM MgCl ₂	4 μ l 25 mM MgCl ₂
8 μ l 10X PCR buffer II	8 μ l 10X Vent PCR buffer
65.5 μ l di DEPC water	65.5 μ l di DEPC water
0.5 μ l AmpliTaq polymerase	0.5 μ l Vent polymerase

After 1 minute and 35 seconds at 95°C, 1 μ l each of 15 μ M stocks of the upstream and downstream primers (BXK33 and BXK34) were added to the PCR reaction (100 μ l total PCR reaction volume) and the PCR reaction solutions were subjected to 35 cycles (95°C for 15 seconds, then 60°C for 30 seconds). The amplified PCR reaction was then maintained at 72°C for 7 minutes and then stored at 4°C. An amplification positive control reaction was carried out under the same conditions with DM151 and DM152 primers.

DM151

(SEQ ID 30): 5'-GTCTCTGAATCAGAAATCCTTCTATC-3'

DM152 (SEQ ID 31): 5'-CATGTCAAATTTCACTGCTTCATCC-3'

25

Electrophoresis of the nucleic acid solutions after PCR amplification displayed an amplification product corresponding approximately to the size of the desired 1.445

Kb structural gene. The fragment was cloned into an M13 vector. A representative sequencing reaction consisted of: 10 µl of plasmid DNA (200-500 ng), 2 µl of M13 Forward or Reverse primer (15 picomoles) and 8 µl of Big Dye Terminator
5 Reaction Mix (PE Applied Biosci.). The clone copy of ATA101105 was called CPR17398. The sequence of the selected clone (*Arabidopsis* obtusifoliol C14α-demethylase) is identified as SEQ ID NO:9.

The predicted polypeptide sequence for the cloned
10 *Arabidopsis* obtusifoliol C14α-demethylase sequence was subjected to a BLAST search in the public database and found to align with the sorghum obtusifoliol 14-alpha demethylase polypeptide (ATA101105/U74319/g1658192; and g1216657/U74319) exhibiting 75-78% sequence identity and 87-90% sequence
15 homology. The cloned nucleic acid encoding *Arabidopsis* obtusifoliol C14α-demethylase (SEQ ID No:9) is missing the 5' end.

The 5' terminal portion of the structural gene was obtained by the RACE (Rapid Amplification of cDNA Ends) PCR
20 using primers BXK39 and BXK40 per manufacturer's instructions (Clontech).

BXK39 (SEQ ID 32): 5'-GAGATCTCCACAGATTTAAAGAACCCTAACG-3'

25 BXK40 (SEQ ID 33): 5'-GGAGCTCGGTTTTTAAGAAAAGGGACGACGC-3'

The cloned nucleic acid encoding full length
Arabidopsis obtusifoliol C14α-demethylase is identified as
SEQ ID No:8. The amplified *Arabidopsis* obtusifoliol C14α-
30 demethylase structural gene is useful for making constructs that express *Arabidopsis* obtusifoliol C14α-demethylase in transgenic plants.

In light of the detailed description of the invention and the examples presented above, it can be appreciated that the several aspects of the invention are achieved.

It is to be understood that the present invention has
5 been described in detail by way of illustration and example in order to acquaint others skilled in the art with the invention, its principles, and its practical application. Particular formulations and processes of the present invention are not limited to the descriptions of the
10 specific embodiments presented, but rather the descriptions and examples should be viewed in terms of the claims that follow and their equivalents. While some of the examples and descriptions above include some conclusions about the way the invention may function, the inventor does not intend
15 to be bound by those conclusions and functions, but puts them forth only as possible explanations.

It is to be further understood that the specific embodiments of the present invention as set forth are not intended as being exhaustive or limiting of the invention,
20 and that many alternatives, modifications, and variations will be apparent to those of ordinary skill in the art in light of the foregoing examples and detailed description. Accordingly, this invention is intended to embrace all such alternatives, modifications, and variations that fall within
25 the spirit and scope of the following claims.

WHAT IS CLAIMED IS:

1. A recombinant construct comprising:
 - (a) a DNA sequence encoding a polypeptide having 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity, and
 - 5 (b) a DNA sequence encoding at least one polypeptide having steroid pathway enzyme activity selected from the group consisting of:
 - squalene epoxidase enzyme activity,
 - sterol methyl transferase I enzyme activity,
 - 10 sterol C4-demethylase enzyme activity,
 - obtusifoliol C14 α -demethylase enzyme activity,
 - sterol C5-desaturase enzyme activity, and
 - sterol methyl transferase II enzyme activity.
2. The recombinant construct of claim 1, further comprising at least one promoter operably linked to said coding regions.
3. The recombinant construct of claim 1, further comprising a first promoter operably linked to said DNA sequence encoding a polypeptide having 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity and
5 a second promoter operably linked to said DNA sequence encoding at least one polypeptide having steroid pathway enzyme activity, wherein said first and second promoters may or may not be the same.
4. The recombinant construct of claim 2 or 3 further comprising an operably linked transcription termination sequence located 3' to each coding region.

5. A recombinant construct according to claim 3 wherein the promoters are selected from the group consisting of seed-specific promoters, organ specific promoters and constitutive promoters.

6. A recombinant vector comprising operably linked in the 5' to 3' direction,

a promoter, a DNA sequence encoding a polypeptide having 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity, and a transcription termination signal sequence;

a promoter, a DNA sequence encoding at least one polypeptide having steroid pathway enzyme activity selected from the group consisting of

10 squalene epoxidase enzyme activity,
sterol methyl transferase I enzyme activity,
sterol C4-demethylase enzyme activity,
obtusifoliol C14 α -demethylase enzyme activity,
sterol C5-desaturase enzyme activity, and
15 sterol methyl transferase II enzyme activity,
and a transcription termination signal sequence.

7. The recombinant vector of claim 6 wherein said vector is a plant expression vector.

8. A transformed host cell comprising a recombinant construct of claim 1.

9. The transformed host cell of claim 8 wherein said cell is a plant cell.

10. A transformed host cell comprising a recombinant vector of claim 6.

11. The transformed host cell according to claim 10 wherein said host cell is a plant cell.

12. A transformed host cell comprising a plant expression vector comprising:

- (a) as operably linked components in the 5' to 3' direction, a promoter, a DNA sequence encoding a polypeptide having 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity, and a transcription termination signal sequence; and
- (b) as operably linked components in the 5' to 3' direction, a promoter, a DNA sequence encoding at least one polypeptide having steroid pathway enzyme activity selected from the group consisting of
 - squalene epoxidase enzyme activity,
 - sterol methyl transferase I enzyme activity,
 - sterol C4-demethylase enzyme activity,
 - obtusifoliol C14 α -demethylase enzyme activity,
 - sterol C5-desaturase enzyme activity, and
 - sterol methyl transferase II enzyme activity, anda transcription termination signal sequence.

13. The transformed host cell according to claim 12 wherein said host cell is a plant cell.

14. A cell culture comprising transformed host cells according to any of claims 8-13.

15. A plant comprising at least one transformed host cell of any of claims 8-13.

16. A plant according to claim 15 wherein said transformed host cell comprises a plant cell.

17. A storage organ, comprising at least one transformed host cell according to any one of claims 8-13.

18. A storage organ including at least one transformed host cell containing a recombinant vector comprising:

- (a) as operably linked components in the 5' to 3' direction, a promoter, a DNA sequence encoding at least one polypeptide having 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity, and a transcription termination signal sequence; and
- (b) as operably linked components in the 5' to 3' direction, a promoter, a DNA sequence encoding a polypeptide having steroid pathway enzyme activity selected from the group consisting of
 - squalene epoxidase enzyme activity,
 - sterol methyl transferase I enzyme activity,
 - sterol C4-demethylase enzyme activity,
 - obtusifoliol C14 α -demethylase enzyme activity,
 - sterol C5-desaturase enzyme activity, and
 - sterol methyl transferase II enzyme activity, anda transcription termination signal sequence.

19. The storage organ according to claim 18 wherein said recombinant vector is a plant expression vector.

20. A process of increasing the formation of steroid pathway products in a transformed host cell as compared to an otherwise identical non-transformed host cell comprising:

5 (1) transforming a host cell with a recombinant vector comprising

(a) as operably linked components in the 5' to 3' direction, a promoter, a DNA sequence encoding a first polypeptide having
10 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity, and a transcription termination signal sequence; and

(b) as operably linked components in the 5' to 3' direction, a promoter, a DNA sequence encoding at least one polypeptide having steroid pathway enzyme activity
15 selected from the group consisting of

squalene epoxidase enzyme activity,
20 sterol methyl transferase I enzyme activity,

sterol C4-demethylase enzyme activity,
obtusifoliol C14 α -demethylase enzyme activity,

25 sterol C5-desaturase enzyme activity, and

sterol methyl transferase II enzyme activity,

30 and a transcription termination signal sequence, and

(2) regenerating said transformed plant cell into said transgenic plant.

21. The process according to claim 20 wherein said first encoded polypeptide comprises the catalytic region and at least a portion of the linker region but is free from the membrane binding region of an 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme.

22. The process according to claim 20 wherein said promoters are promoters whose regulatory function is substantially unaffected by levels of squalene in said transgenic plant.

23. The process according to claim 20 wherein said plant cell is selected from the group consisting of canola, soybean, corn, tobacco, cotton, tomato, potato, safflower, sunflower, peanut, rape, flax, oil palm, cuphea and alfalfa.

24. A transgenic plant produced in accordance with the process of claim 20.

25. A transgenic plant seed transformed with a vector comprising a DNA segment that encodes a polypeptide having 3-hydroxy-3-methylglutaryl-Coenzyme A reductase activity, and a DNA segment that encodes a polypeptide having a steroid pathway enzyme activity selected from the group consisting of

squalene epoxidase enzyme activity,
sterol methyl transferase I enzyme activity,
sterol C4-demethylase enzyme activity,
obtusifoliol C14 α -demethylase enzyme activity,
sterol C5-desaturase enzyme activity, and
sterol methyl transferase II enzyme activity,

and a promoter suitable for driving expression of said polypeptides in said plant cell, wherein said
15 transgenic plant seed is capable of germinating into a transgenic plant that over-accumulates steroid pathway products relative to a non-transformed plant of the same strain; and mutants, recombinants, genetically engineered derivatives thereof and hybrids derived
20 therefrom, wherein said mutants, recombinants, genetically engineer derivatives thereof and hybrids derived therefrom maintain the ability to overaccumulate steroid pathway products.

26. A plant, the genome of which includes introduced DNA comprising:

DNA encoding a polypeptide having 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity,
5 wherein said plant contains an elevated level of total accumulated sterol, compared to an otherwise identical plant, the genome of which does not comprise said introduced DNA encoding a polypeptide encoding 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme
10 activity; and
further comprising introduced DNA encoding at least one polypeptide having steroid pathway enzyme activity selected from the group consisting of
squalene epoxidase enzyme activity,
15 sterol methyl transferase I enzyme activity,
sterol C4-demethylase enzyme activity,
obtusifoliol C14 α -demethylase enzyme activity,
sterol C5-desaturase enzyme activity, and
sterol methyl transferase II enzyme activity,
20 wherein said introduced DNAs are operatively linked to regulatory signals that cause seed-specific expression

of said introduced DNAs, and wherein seeds of said plant contain a reduced level of squalene, cycloartenol, 24-methylene cycloartenol, obtusifoliol, stigmasterol, or campesterol compared to the seeds of an otherwise identical plant whose genome does not contain introduced DNA encoding said at least one polypeptide having steroid pathway enzyme activity.

27. A plant, the genome of which includes an introduced DNA sequence encoding a polypeptide having 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity and an introduced DNA sequence encoding at least one polypeptide having squalene epoxidase enzyme activity, sterol methyl transferase I enzyme activity, sterol C4-demethylase enzyme activity, obtusifoliol C14 α -demethylase enzyme activity, sterol C5-desaturase enzyme activity, or sterol methyl transferase II enzyme activity, wherein said introduced DNA is operably linked to regulatory signals that cause seed-specific expression of said introduced DNA, and wherein said plant produces seed having an elevated level of a steroid pathway product, compared to a corresponding transgenic or non-transgenic plant that does not contain said introduced DNA.

28. A plant comprising introduced DNA encoding (i) a polypeptide having 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity and (ii) at least one additional polypeptide having squalene epoxidase enzyme activity, sterol methyl transferase I enzyme activity, sterol C4-demethylase enzyme activity, obtusifoliol C14 α -demethylase enzyme

activity, sterol C5-desaturase enzyme activity, or sterol methyl transferase II enzyme activity,
10 wherein said plant that produces a storage organ having an elevated level of a sterol pathway product compared to a corresponding transgenic or non-transgenic plant that does not contain said introduced DNA.

29. The plant of claim 28, wherein said storage organ contains a reduced level of squalene, cycloartenol, 24-methylene cycloartenol, obtusifoliol, stigmasterol, campesterol, or mixtures thereof, compared to a
5 corresponding transgenic plant that comprises introduced DNA encoding a polypeptide having 3-hydroxy-3-methylglutaryl-Coenzyme A reductase enzyme activity but that does not contain introduced DNA encoding at least one polypeptide having squalene epoxidase enzyme
10 activity, sterol methyl transferase I enzyme activity, sterol C4-demethylase enzyme activity, obtusifoliol C14 α -demethylase enzyme activity, sterol C5-desaturase enzyme activity, sterol methyl transferase II enzyme activity.

30. The plant of any one of claims 24 to 29, wherein said regulatory signals cause seed-specific expression of said introduced DNAs.

31. A seed of a plant according to any one of claims 24 to 30.

32. Progeny of a plant according to any one of claims 24 to 30.

33. A plant cell or transformed plant cell of a plant according to any one of claims 24 to 30.

34. A cell culture, comprising cells according to claim 33.

35. A plant produced from a seed according to claim 31.

36. A method of producing a plant comprising sexually crossing a plant according to any one of claims 15, 16 or 24-30 with a non-transformed plant.

37. A plant produced by the method of claim 36.

38. A plant according to any one of claims 24 to 30, wherein said plant is an apomictic plant.

39. A seed resulting from a cross of the plant of claim 38 with a nurse cultivar.

40. A uniform population of plants according to any one of claims 15, 16, 24-30, 37 or 38.

41. Seed of a plant produced by the method of claim 36.

42. A part, other than a seed, of a plant according to any one of claims 15, 16, 24-30, 37 or 38.

43. Oil containing at least one sterol pathway product, extracted from seed of a plant according to any one of claims 15, 16, 24-30, 37 or 38.

44. Oil according to claim 43, wherein sitosterol, at least one sitosterol ester, or mixtures thereof, comprise at least about 57% by weight of the total sterol compounds of said oil.

45. Oil according to claim 43, wherein sitosterol, at least one sitosterol ester, or mixtures thereof, comprise at least about 0.08% of the dry weight of said seed.

46. Oil according to claim 43, having a reduced amount of squalene, cycloartenol, 24-methylene cycloartenol, obtusifoliol, stigmasta-7-enol, campesterol, or mixtures thereof, compared to oil obtained from a
5 corresponding plant that does not contain introduced DNA encoding at least one polypeptide having squalene epoxidase enzyme activity, sterol methyl transferase I enzyme activity, a sterol C4-demethylase enzyme activity, obtusifoliol C14 α -demethylase enzyme
10 activity, sterol C5-desaturase enzyme activity, or sterol methyl transferase II enzyme activity; wherein the reduction is in the range of from about 10% to about 100% .

47. A sitosterol ester composition extracted from seed of a plant according to any one of claims 15, 16, 24-30, 37 or 38.

48. The sitosterol ester composition of claim 47, wherein an esterifying fatty acid has 2 to 22 carbon atoms in the main chain.

49. A cholesterol-lowering composition, comprising said oil of any one of claims 43 to 46.

50. A food, food ingredient, or food composition, comprising said oil of any one of claims 43 to 46.

51. A pharmaceutical composition, comprising a cholesterol-lowering effective amount of said oil of any one of claims 43 to 46, and a pharmaceutically acceptable carrier, excipient, or diluent.

52. A method of lowering the plasma concentration of low density lipoprotein cholesterol, comprising orally administering to a human or animal subject an effective amount of a composition according to any one of claims
5 49-51.

53. A method of treating or preventing an elevated plasma concentration of low density lipoprotein cholesterol, comprising orally administering to a human or animal subject an effective amount of a composition
5 according to any one of claims 49-51.

54. A method of making a food additive composition, comprising:
obtaining oil containing a sterol pathway product compound from seed of a transgenic plant according to
5 any one of claims 15, 16, 24-30, 37 or 38; and
mixing said oil with an edible solubilizing agent, a dispersant, and optionally, an antioxidant.

55. An isolated DNA molecule, having a nucleotide sequence selected from the group consisting of:

- (a) disclosure squalene epoxidase SEQ ID NO:4, 6, 8, 10, or the complement thereof;
- 5 (b) a nucleotide sequence that hybridizes to said nucleotide sequence of (a) under a wash stringency equivalent to 0.5X SSC to 2X SSC, 0.1% SDS, at 55-65°C, and which encodes a polypeptide having squalene epoxidase enzymatic activity substantially similar to
- 10 that of the disclosed squalene epoxidase;
- (c) a nucleotide sequence encoding the same genetic information as said nucleotide sequence of (a), but which is degenerate in accordance with the degeneracy of the genetic code; and
- 15 (d) a nucleotide sequence encoding the same genetic information as said nucleotide sequence of (b), but which is degenerate in accordance with the degeneracy of the genetic code.

56. An isolated DNA molecule, having a nucleotide sequence selected from the group consisting of:

- (a) disclosure obtusifoliol C14 α -demethylase SEQ ID NO:12, 14, or 17, or the complement thereof;
- 5 (b) a nucleotide sequence that hybridizes to said nucleotide sequence of (a) under a wash stringency equivalent to 0.5X SSC to 2X SSC, 0.1% SDS, at 55-65°C, and which encodes a polypeptide having obtusifoliol C14 α -demethylase enzymatic activity substantially
- 10 similar to that of the disclosed obtusifoliol C14 α -demethylase;
- (c) a nucleotide sequence encoding the same genetic information as said nucleotide sequence of (a), but which is degenerate in accordance with the degeneracy
- 15 of the genetic code; and

(d) a nucleotide sequence encoding the same genetic information as said nucleotide sequence of (b), but which is degenerate in accordance with the degeneracy of the genetic code.

57. A recombinant construct, comprising as operably linked components in the 5' to 3' direction, a seed-specific promoter, an isolated DNA molecule of claim 55 or 56, and a transcription termination signal sequence.

58. A recombinant vector comprising said recombinant construct of claim 57.

59. The recombinant vector of claim 58, which is a plant expression vector.

60. A transformed host cell, comprising said recombinant construct of claim 57.

61. The transformed host cell of claim 60, wherein said host cell is a plant cell.

62. A method of producing squalene epoxidase or obtusifoliol C14 α -demethylase, comprising culturing a transformed host cell of claim 60 for a time and under conditions conducive to the production of said squalene epoxidase or obtusifoliol C14 α -demethylase enzyme, and recovering said squalene epoxidase or obtusifoliol C14 α -demethylase produced thereby.

63. The transformed host cell of claim 8, further comprising a recombinant construct encoding a tocopherol synthesis pathway enzyme.

64. The transformed host cell of claim 10, further comprising a recombinant vector encoding a tocopherol synthesis pathway enzyme.

65. The transformed host cell of claim 64, wherein said tocopherol synthesis pathway enzyme is S-adenosylmethionine-dependent γ -tocopherol methyltransferase.

66. The transformed host cell of claim 64, wherein said vectors are plant expression vectors.

67. The storage organ of claim 18, wherein said at least one transformed host cell further contains a recombinant vector comprising as operably linked components, a promoter, a DNA sequence encoding a
5 tocopherol synthesis pathway enzyme and a transcription termination sequence.

68. The storage organ of claim 18, wherein said tocopherol synthesis enzyme is S-adenosylmethionine-dependent γ -tocopherol methyltransferase.

69. A process of increasing the formation of steroid pathway products and tocopherols in a transformed host cell as compared to an otherwise identical non-transformed host cell comprising,

- 5 (A) transforming a host cell with:
- (1) a recombinant vector comprising
- (a) as operably linked components in the 5' to 3' direction, a promoter, a DNA sequence encoding a first polypeptide having 3-hydroxy-3-methylglutaryl-Coenzyme
- 10 A reductase enzyme activity, and a transcription termination signal sequence; and
- (b) as operably linked components in the 5' to 3' direction, a promoter, a DNA sequence encoding at least one polypeptide having steroid pathway enzyme activity
- 15 selected from the group consisting of
- squalene epoxidase enzyme activity,
- sterol methyl transferase I enzyme activity,
- sterol C4-demethylase enzyme activity,
- obtusifoliol C14 α -demethylase enzyme activity,
- 20 sterol C5-desaturase enzyme activity, and
- sterol methyl transferase II enzyme activity,
- and a transcription termination signal sequence;
- (2) a recombinant vector comprising as operably linked components, a promoter, a DNA sequence encoding at
- 25 least one tocopherol synthesis pathway enzyme selected from the group consisting of
- 3-deoxy-D-arabino-heptulosonate-7-P synthase (DAHP synthase),
- shikimate kinase,
- 30 a prephenate dehydrogenase,
- 1-deoxy-d-xylulose 5-phosphate synthetase (DXS),
- 1-deoxy-d-xylulose 5-phosphate reductoisomerase (DXR),
- 4-diphosphocytidyl-2C-methyl-d-erythritol synthase (YgbP),
- 35 4-diphosphocytidyl-2C-methyl-d-erythritol kinase (YchB),

2C-methyl-d-erythritol 2,4-cyclodiphosphate synthase
(YgbB),
the gene product of GcpE, LytB,
40 geranylgeranylpyrophosphate synthase (GGPPS),
geranylgeranylpyrophosphate hydrogenase (GGH),
phytyl/prenyltransferase (PPT),
4-hydroxy-phenylpyruvate dioxygenase (HPPD),
2-methyl-6-phytylplastoquinol,
45 tocopherol methyltransferase I (MTI),
tocopherol cyclase and
 γ -tocopherol methyltransferase (GMT);
4-amino-4-deoxyphenate dehydrogenase (TryA);
slr 1736;
50 slr 1737
ATPT2;
AANT1; and

and a transcription termination sequence; and
55 (B) regenerating said transformed plant cell into said
transgenic plant.

70. The process of claim 69, wherein said tocopherol
synthesis enzyme is S-adenosylmethionine-dependent γ -
tocopherol methyltransferase.

71. A plant comprising at least one host cell of any
of claims 63-66.

72. A plant produced by the process of claim 69 or 70.

73. An oil from the plant of claim 71 or 72.

74. A seed from the plant of claim 71 or 72.

75. An oil from the seed of claim 74.

76. A plant produced by crossing the plant of any of claims 26-30, 35, 37, or 38 with a plant comprising a recombinant expression vector containing as operably linked components a promoter, a DNA sequence encoding a
5 tocopherol synthesis pathway enzyme, and a transcription termination sequence.

77. The plant of claim 77, wherein said tocopherol synthesis enzyme is S-adenosylmethionine-dependent - tocopherol methyltransferase.

FIG. 1

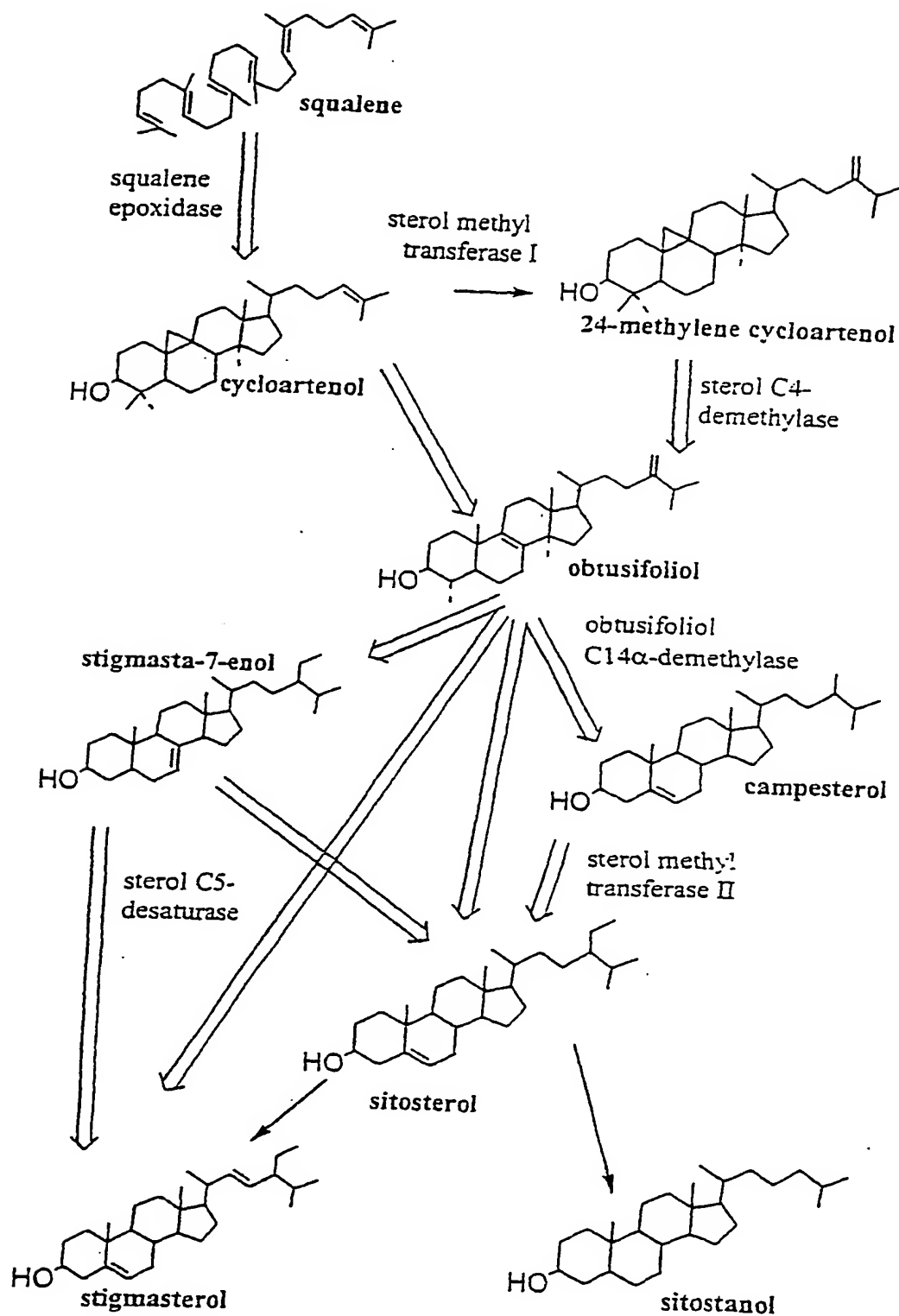
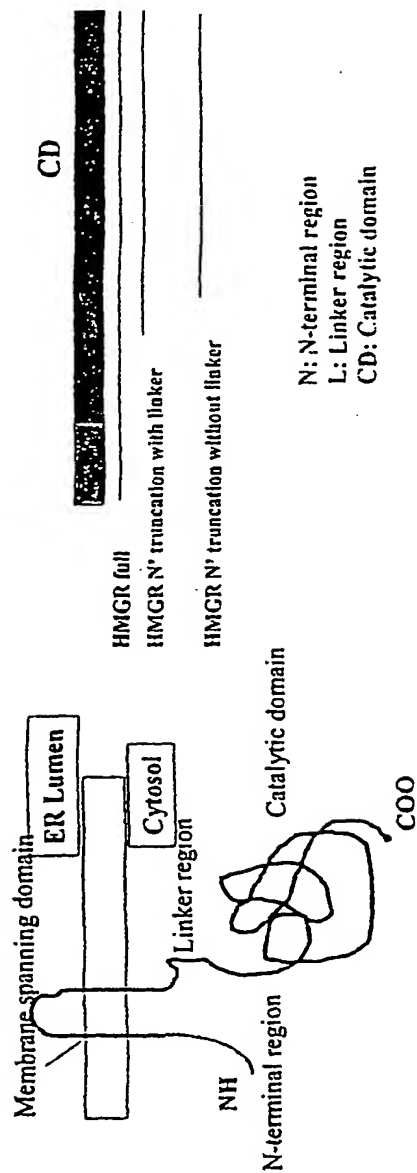


FIG. 2



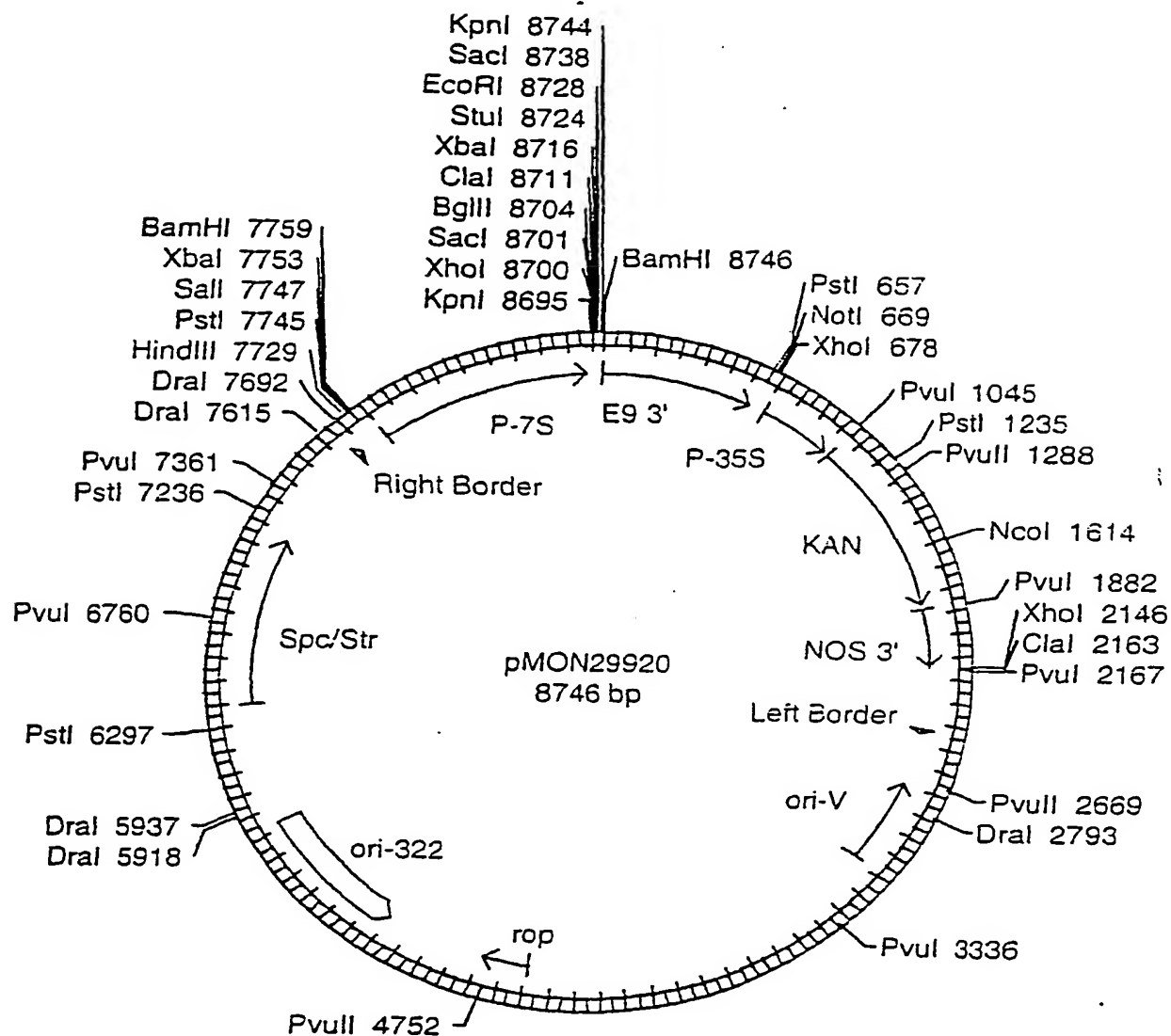


Figure 3: Construct pMON29920

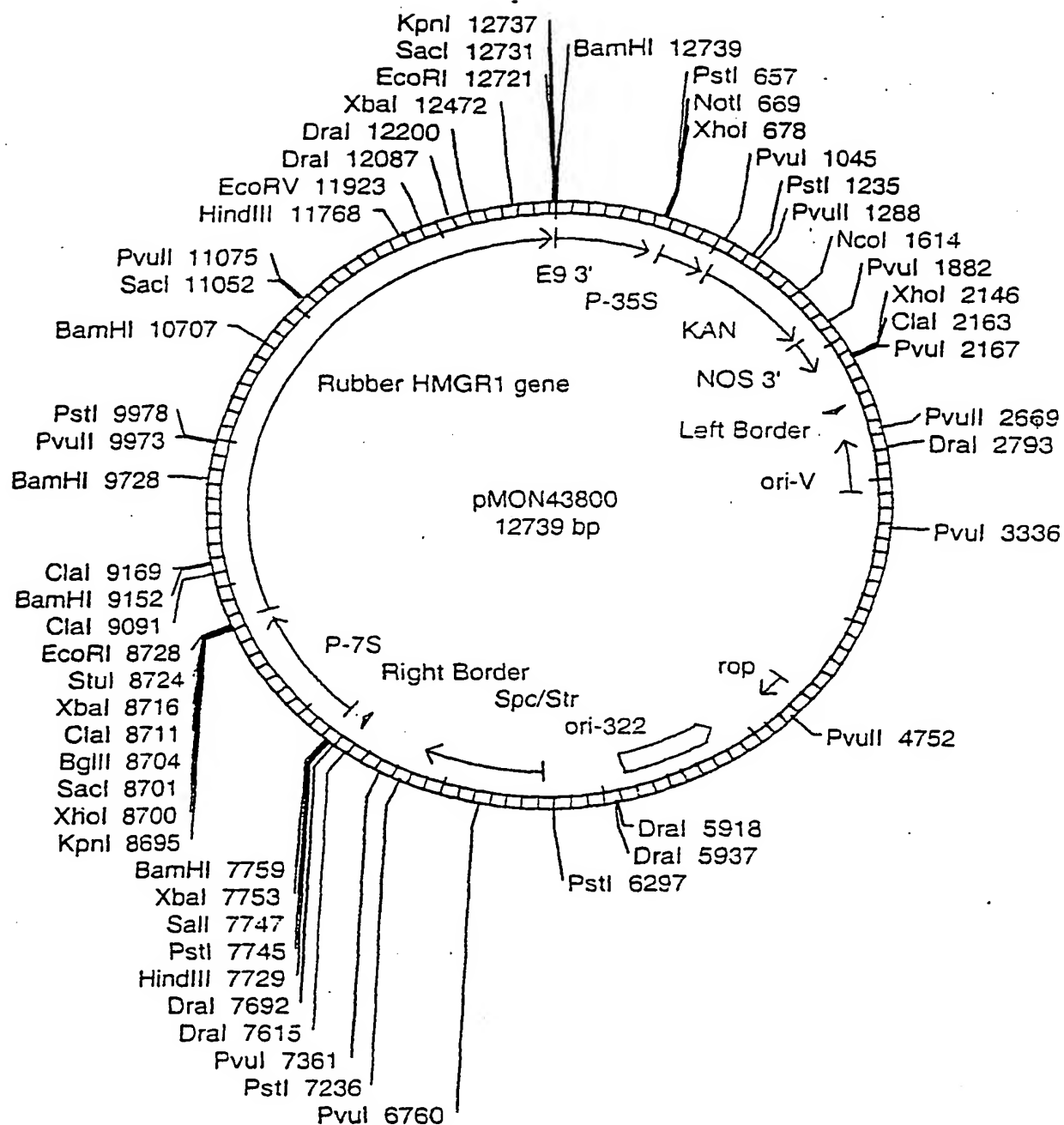


Figure 4: Construct pMON43800

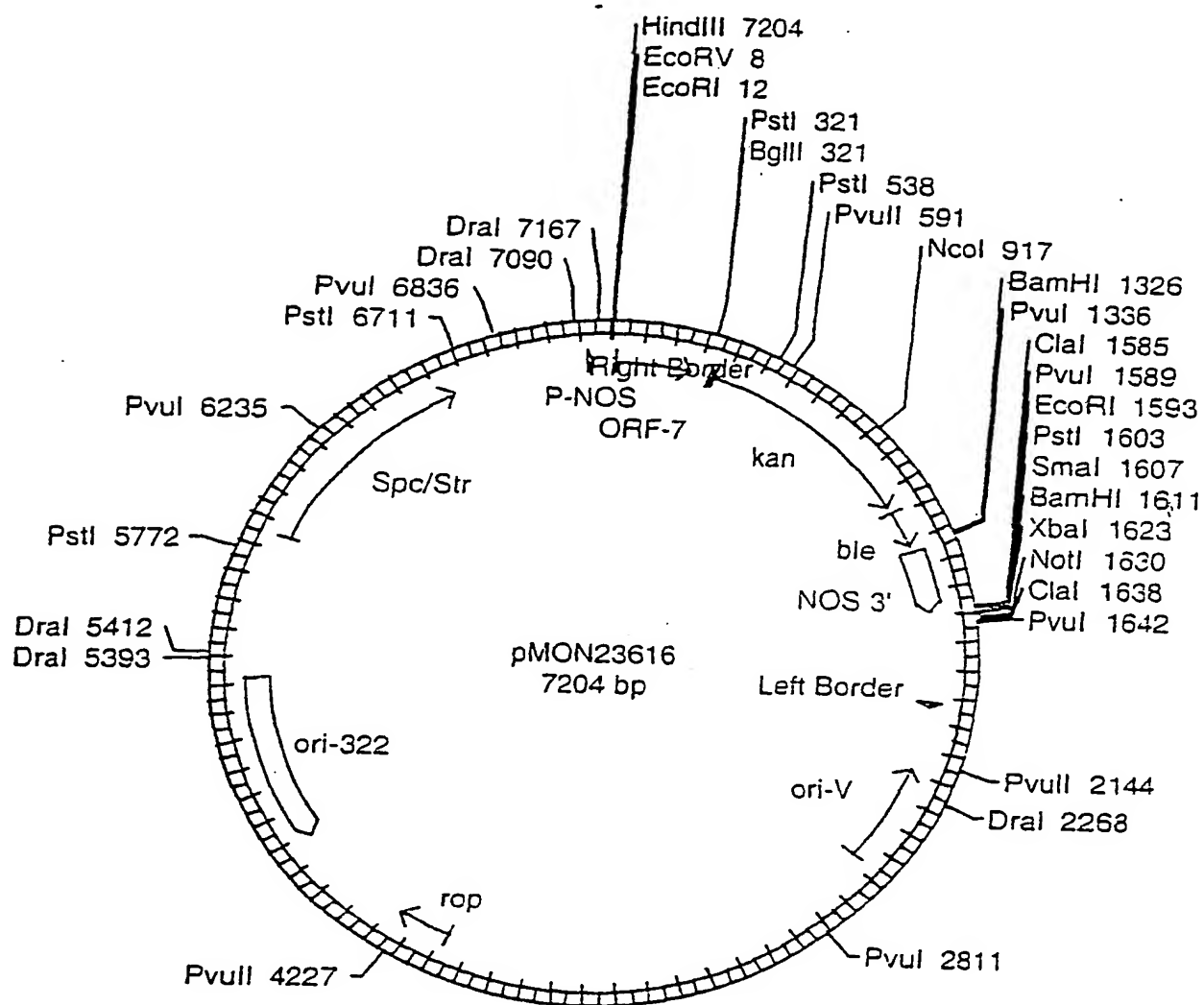


Figure 5: Construct pMON23616

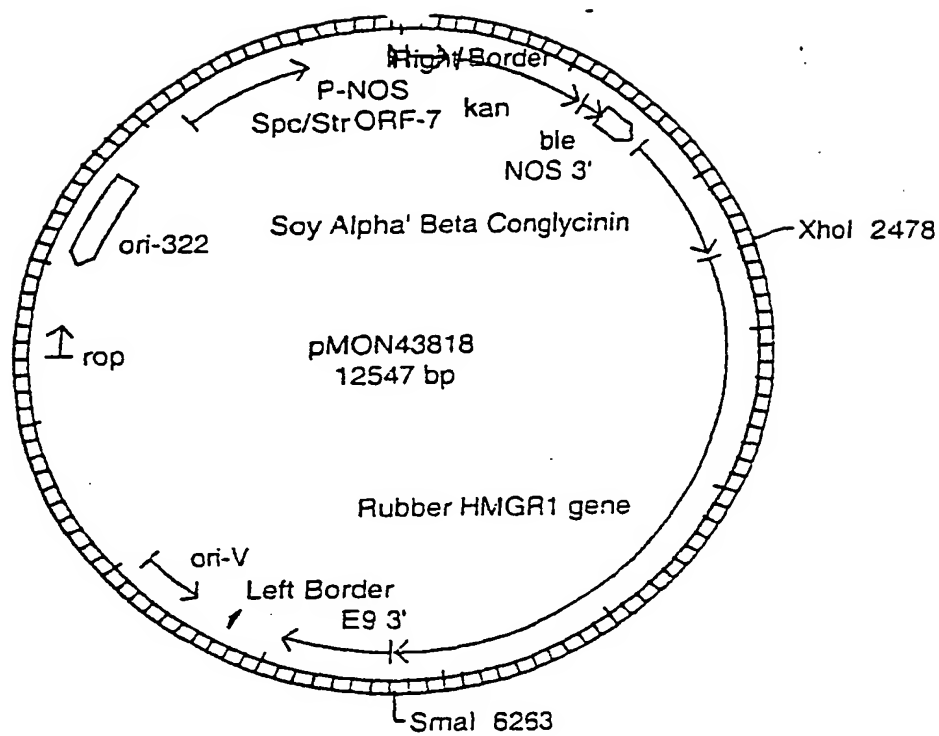


Figure 6: Construct pMON43818

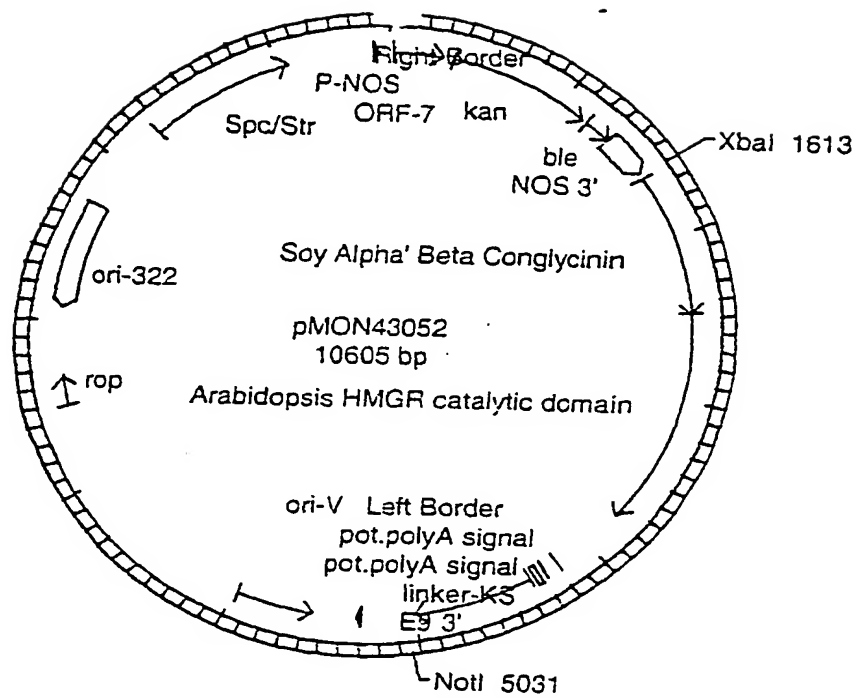


Figure 7: Construct pMON43052

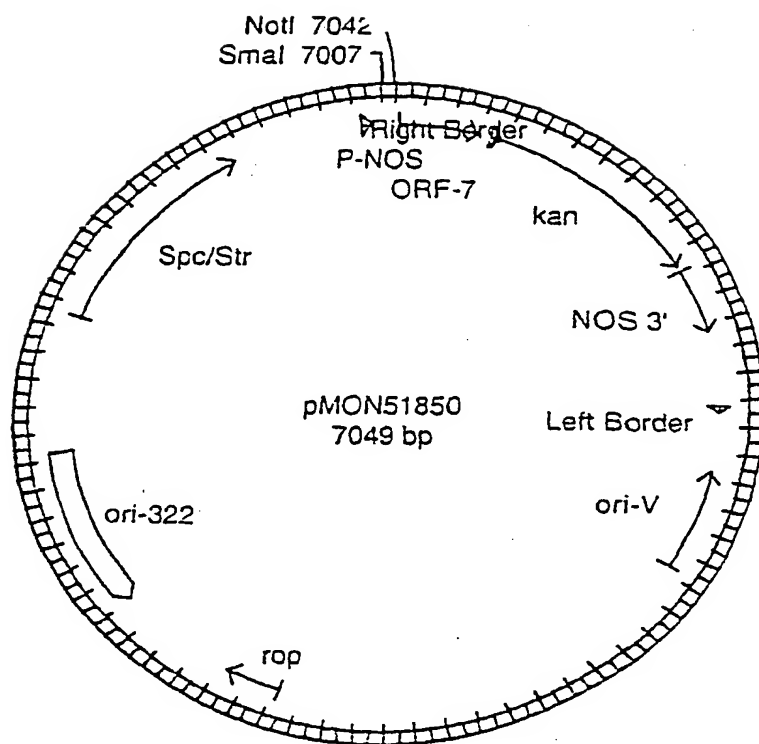


Figure 8: Construct pMON51850

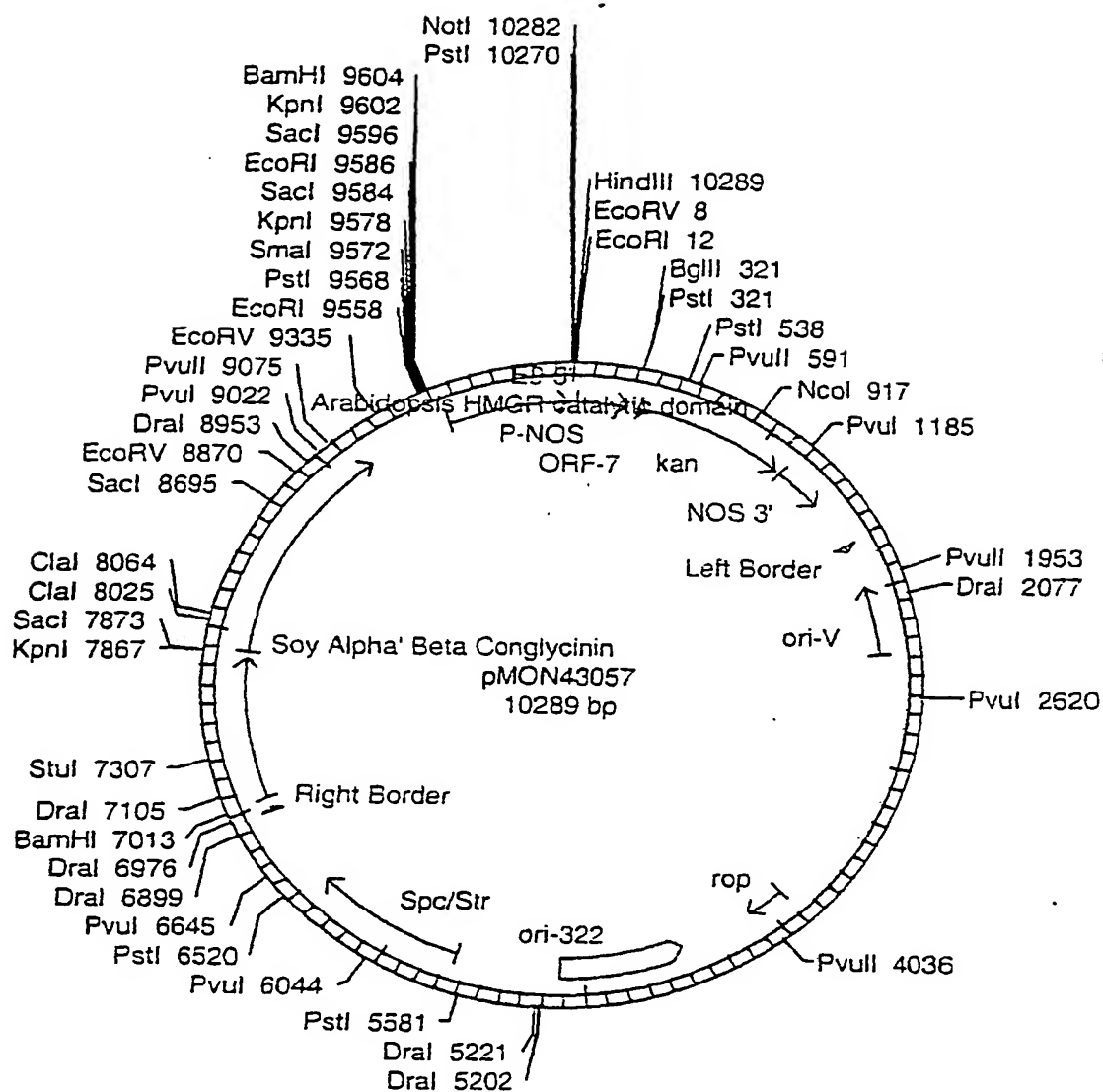


Figure 9: Construct pMON43057

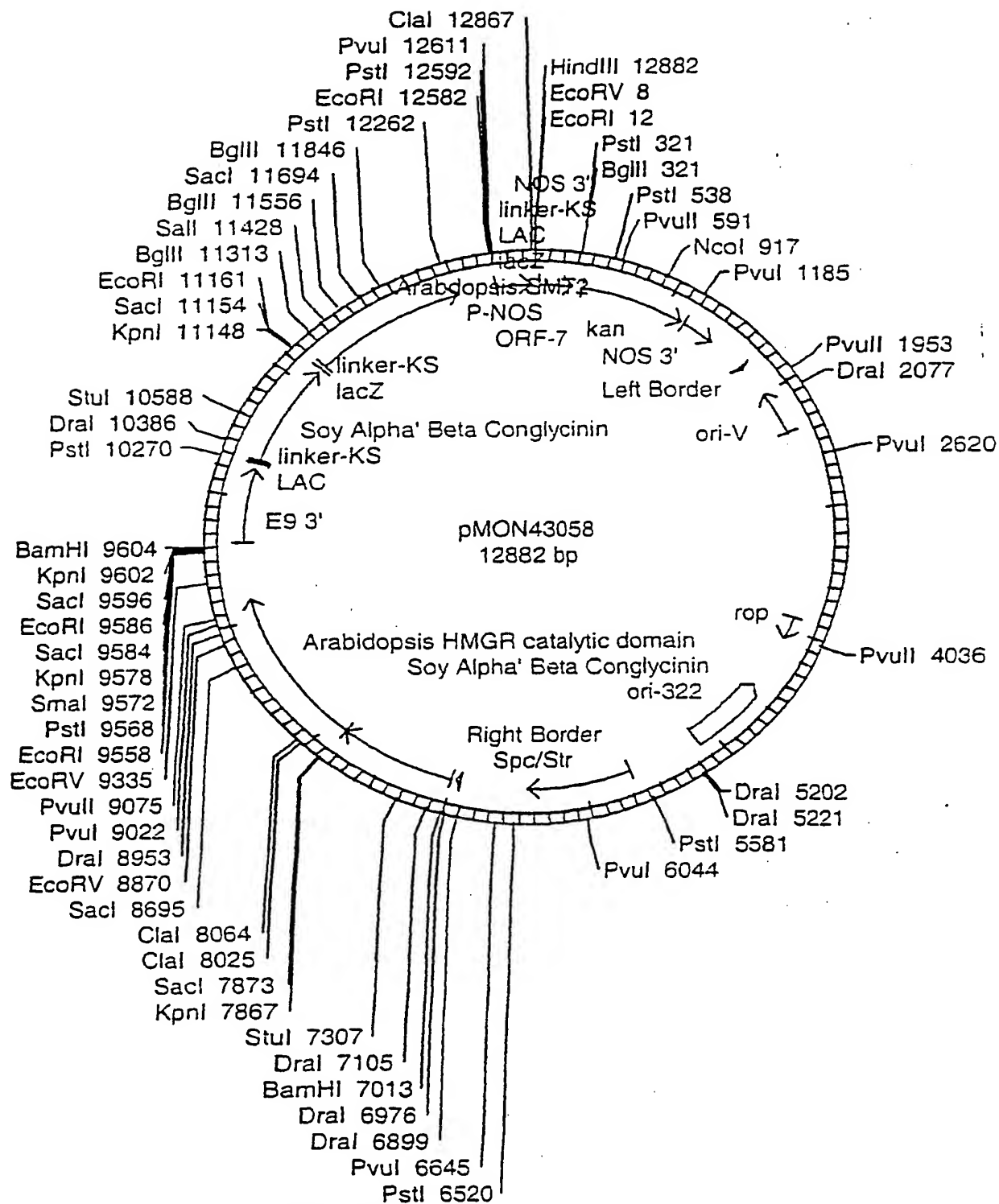


Figure 10: Construct pMION43058

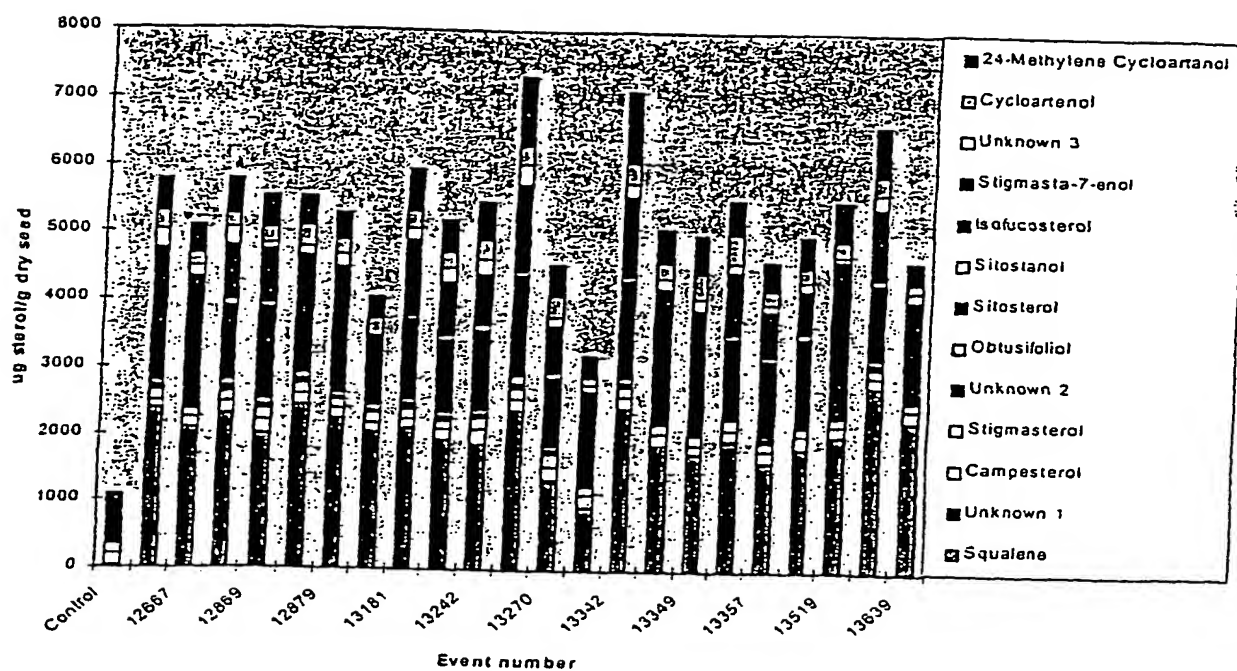


Figure 11: Sterol composition of R1 transgenic soybean seeds when *Arabidopsis* truncated HMGR (catalytic domain without linker) was overexpressed using seed-specific 7S promoter (data from pMON43057: p7s::Ar HMGR truncated).

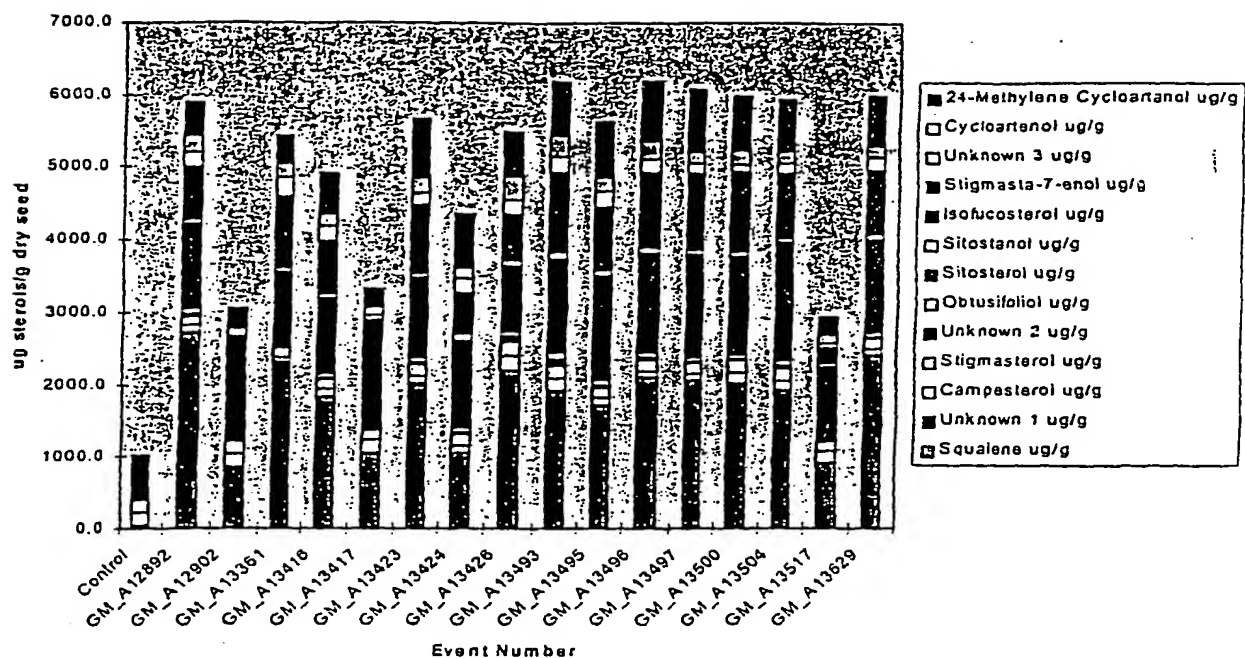


Figure 12: Sterol composition of R1 transgenic soybean seeds when *Arabidopsis* truncated HMGR (catalytic domain without linker) and *Arabidopsis* SMTII were overexpressed (data from pMON43058: p7S::*At* HMGR truncated & p7S::*At* SMTII). The expression of the genes is controlled by the seed-specific 7S promoter.

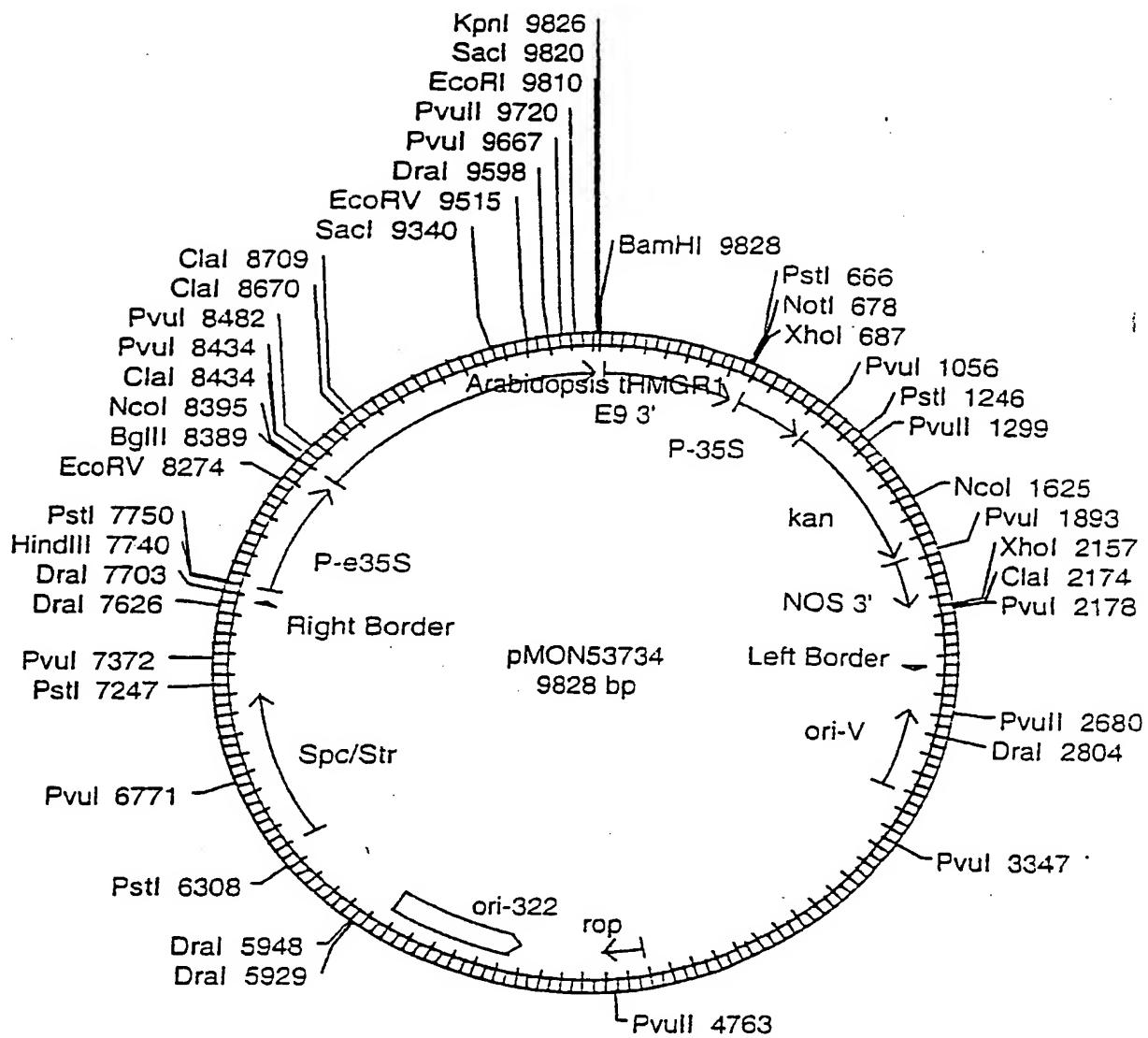


Figure 14: Construct pMON53734

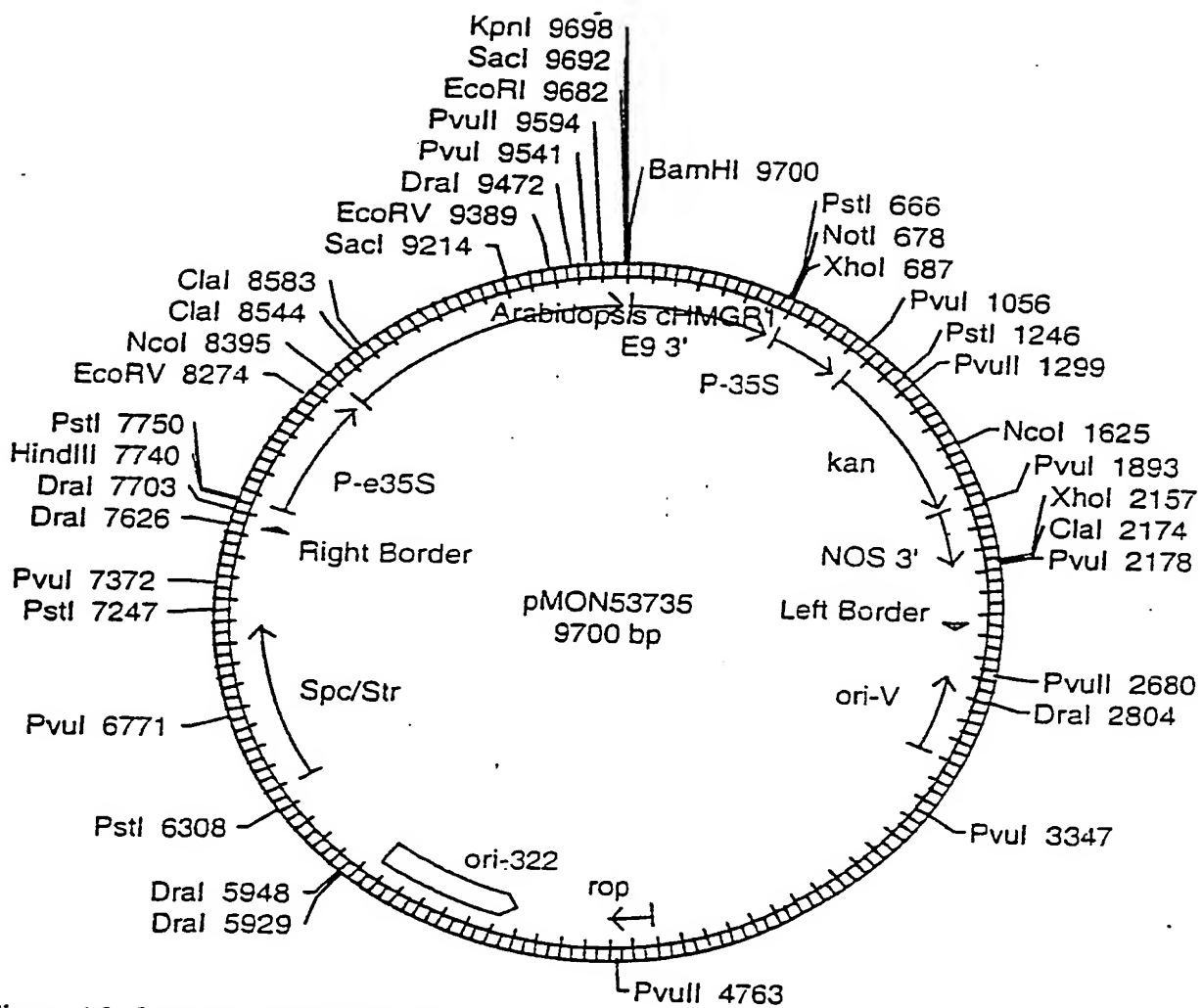


Figure 15: Construct pMON53735

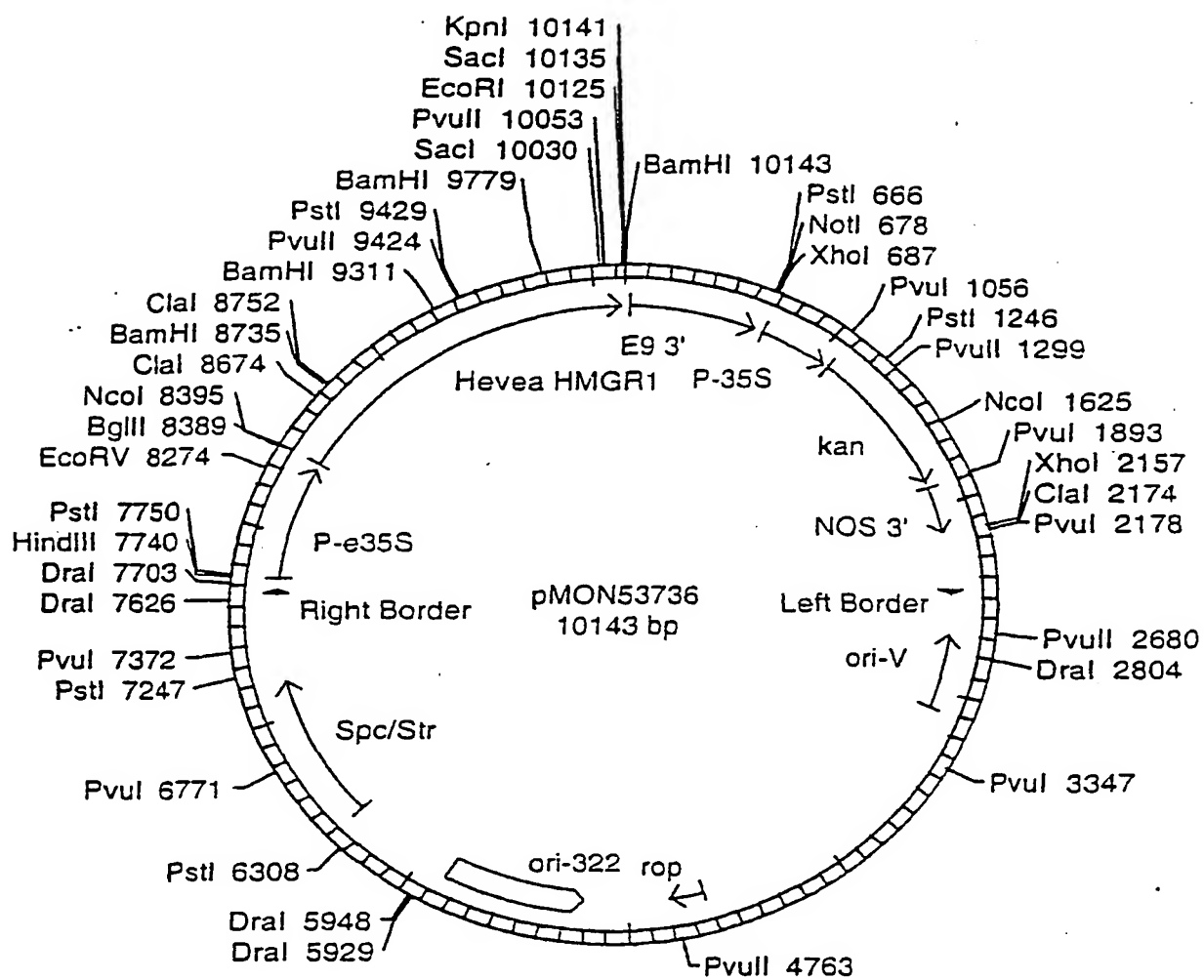


Figure 16: Construct pMON53736

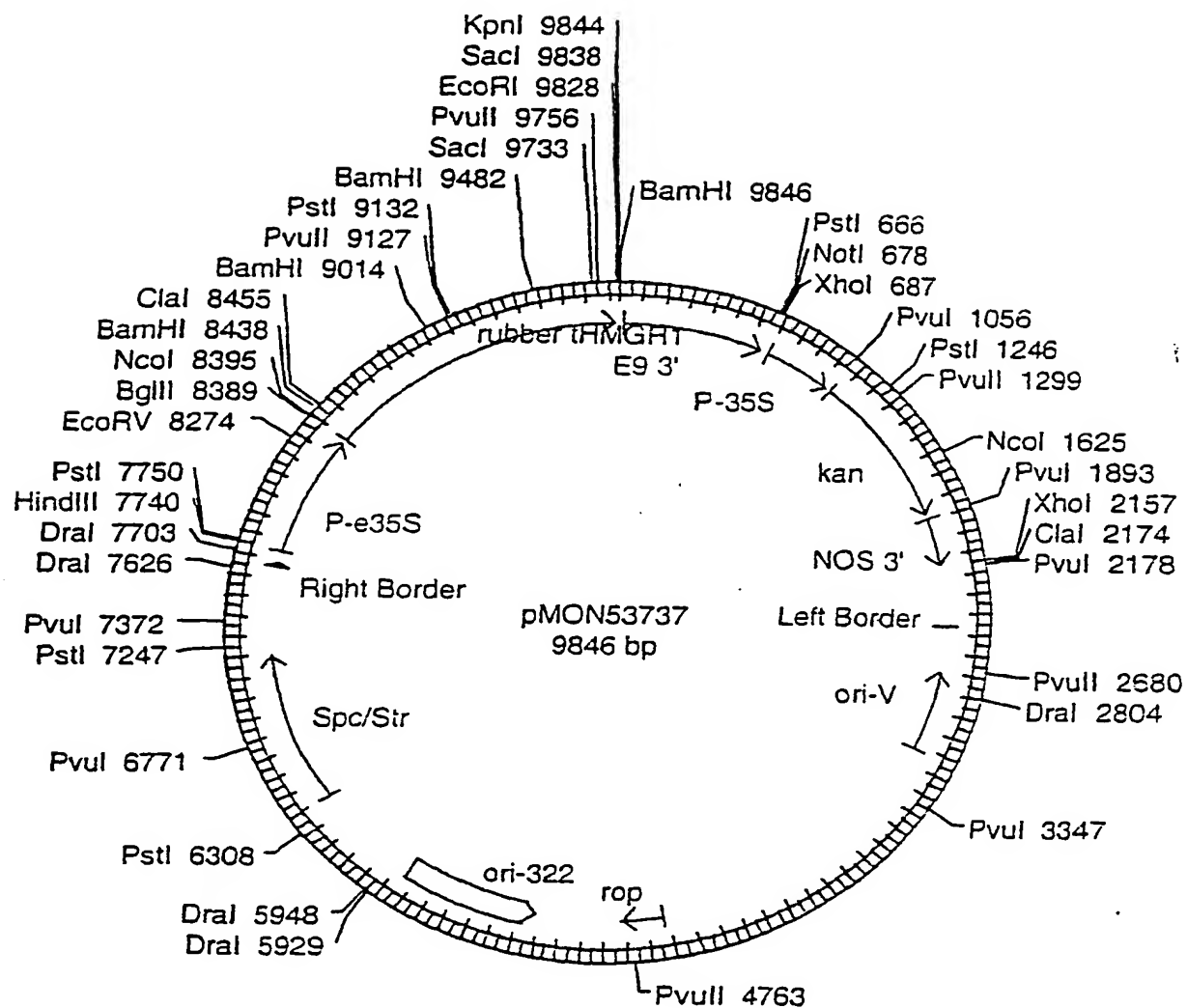


Figure 17: Construct pMON53737

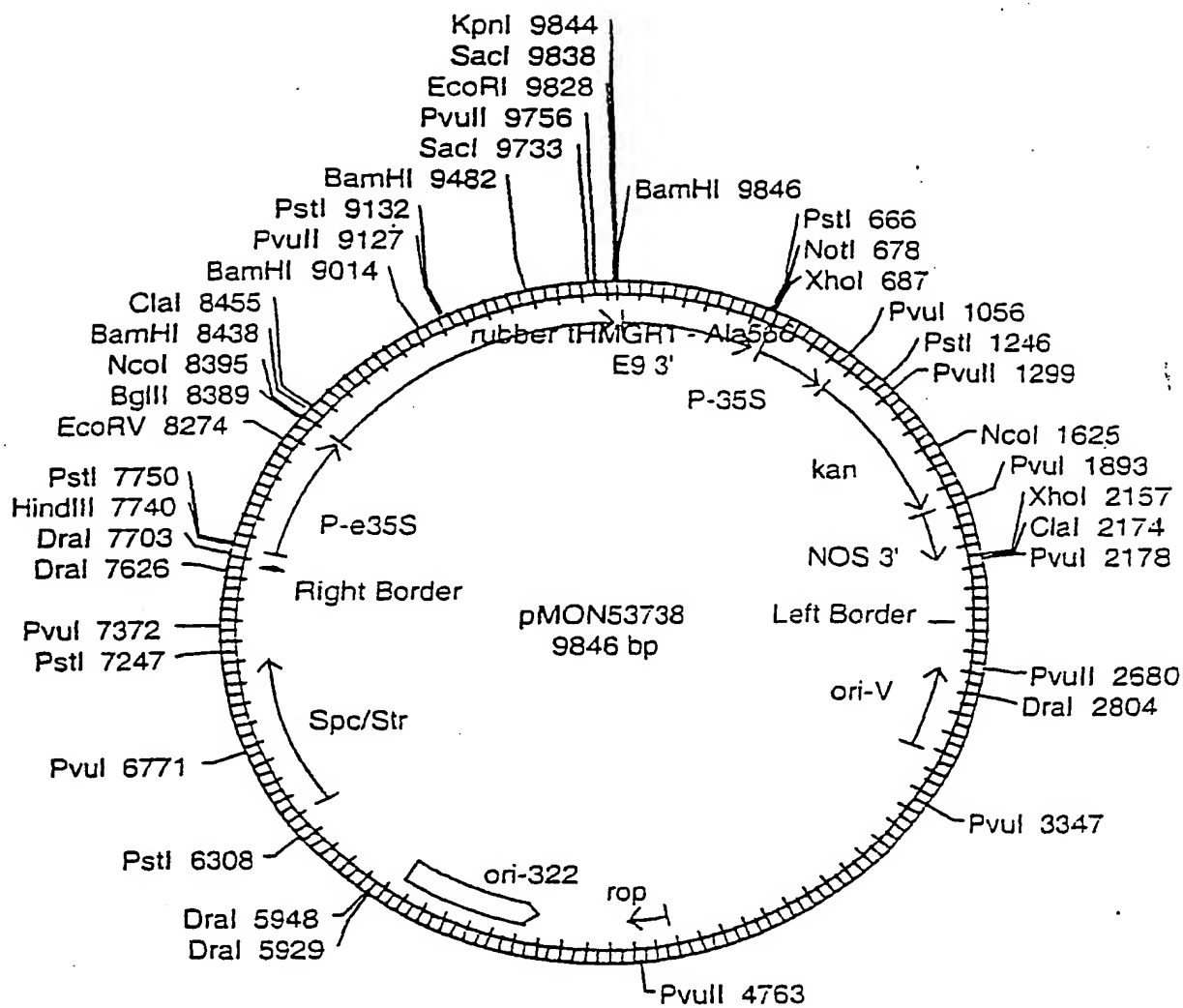


Figure 18: Construct pMON53738

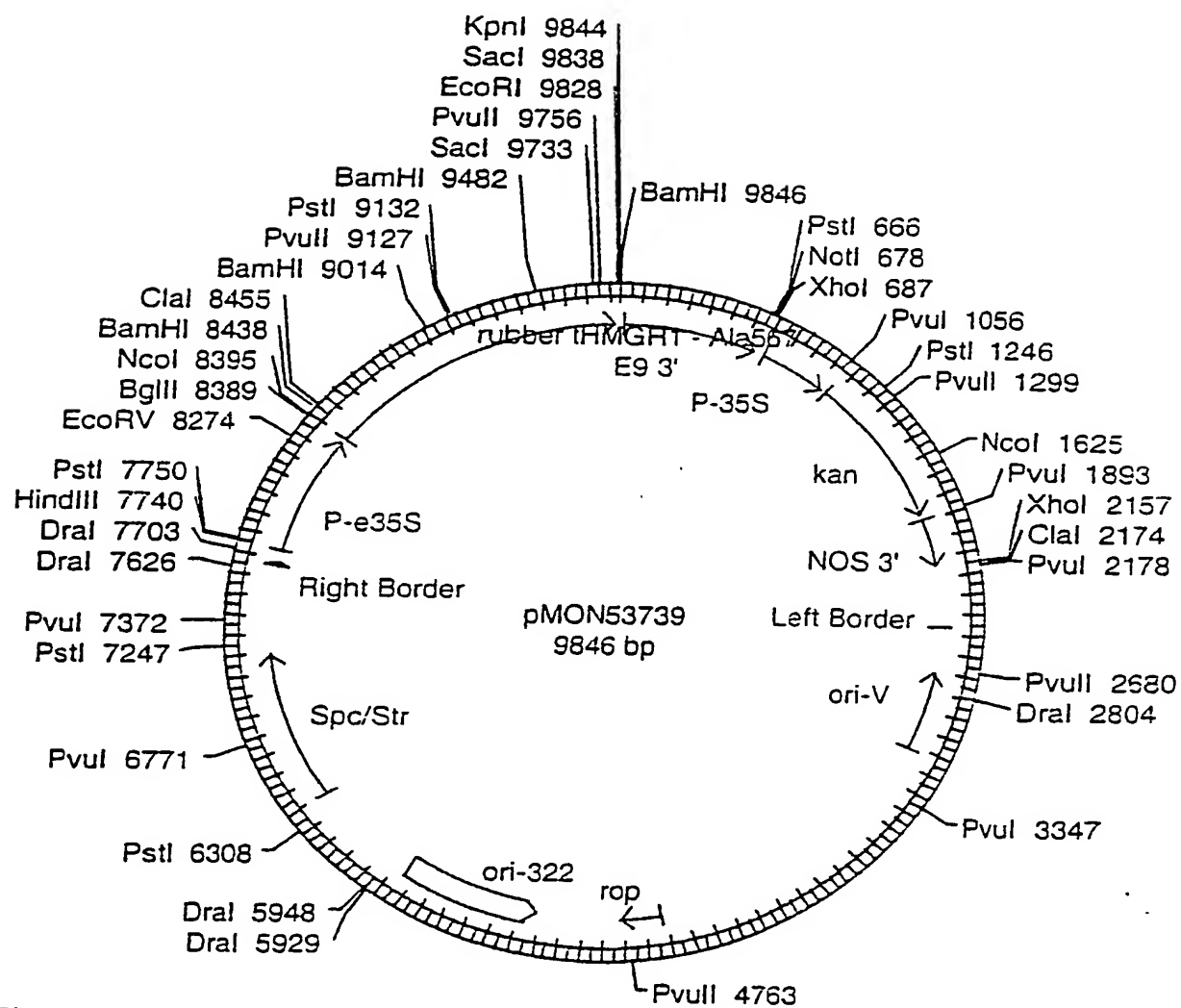


Figure 19: Construct pMON53739

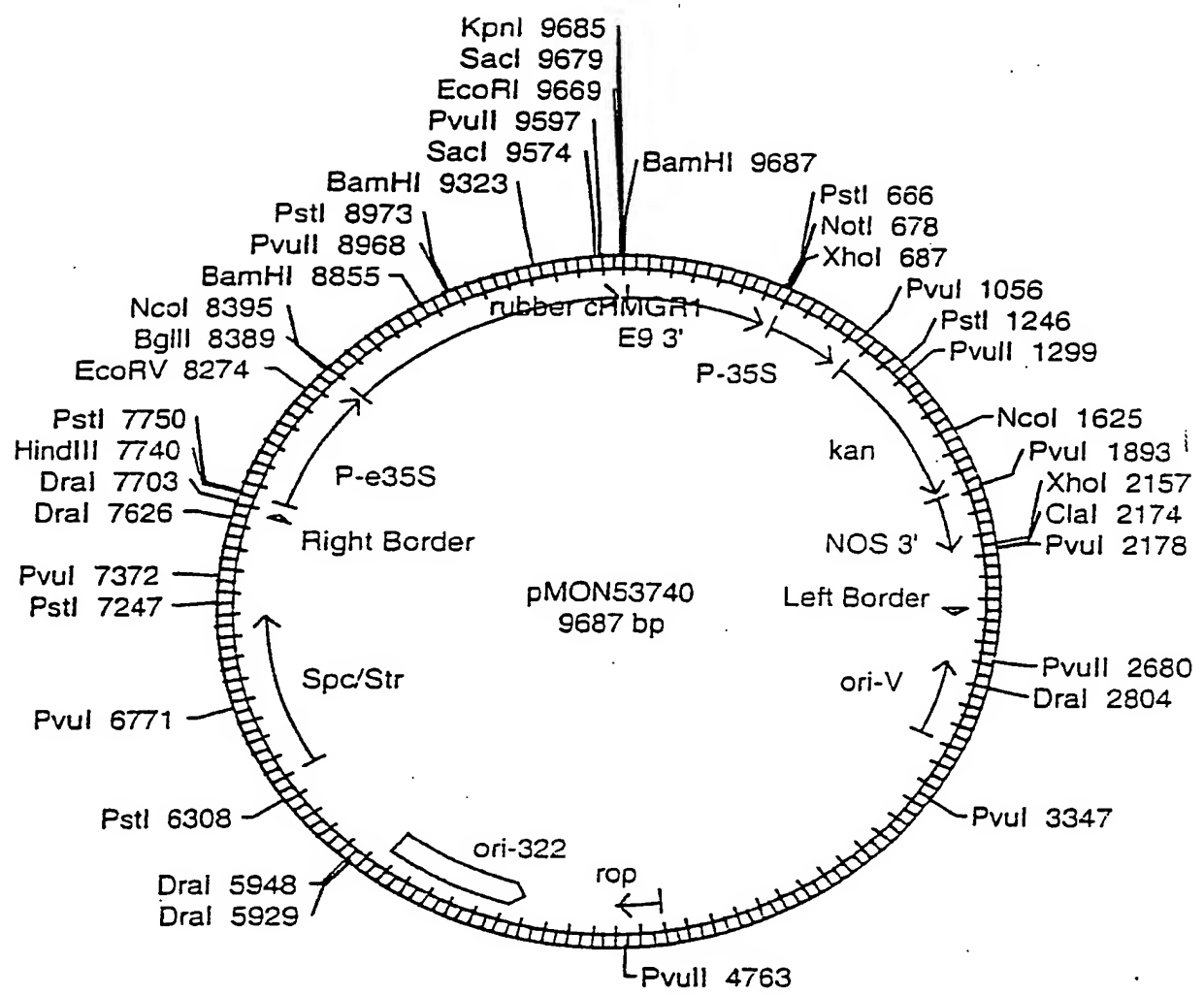


Figure 20: Construct pMON53740

FIG. 21

Comparison of Cycloartenol Levels in Transgenic Plants

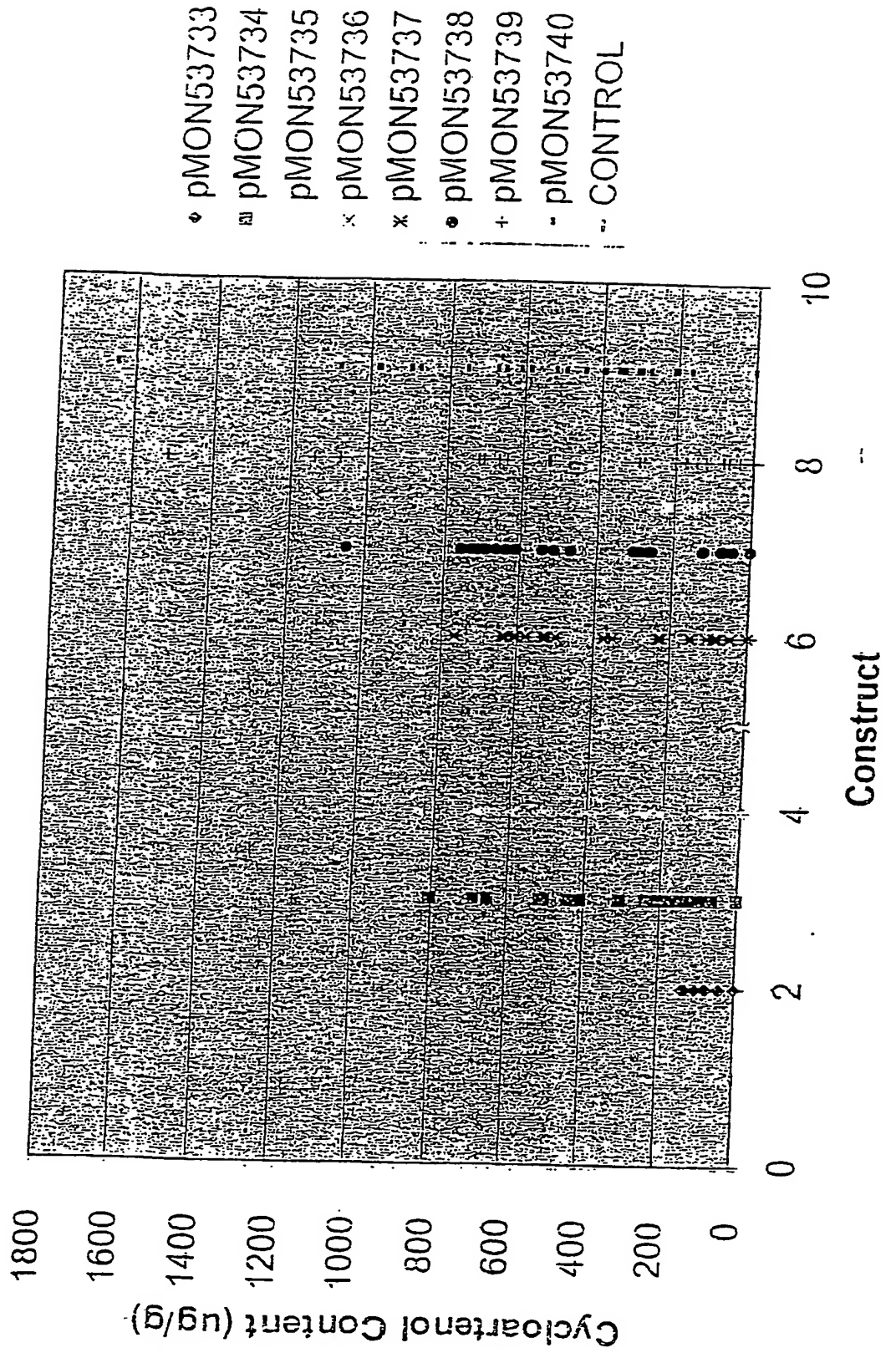


FIG. 22

Comparison of 24-Methylene Cycloartenol in Transgenic Plants

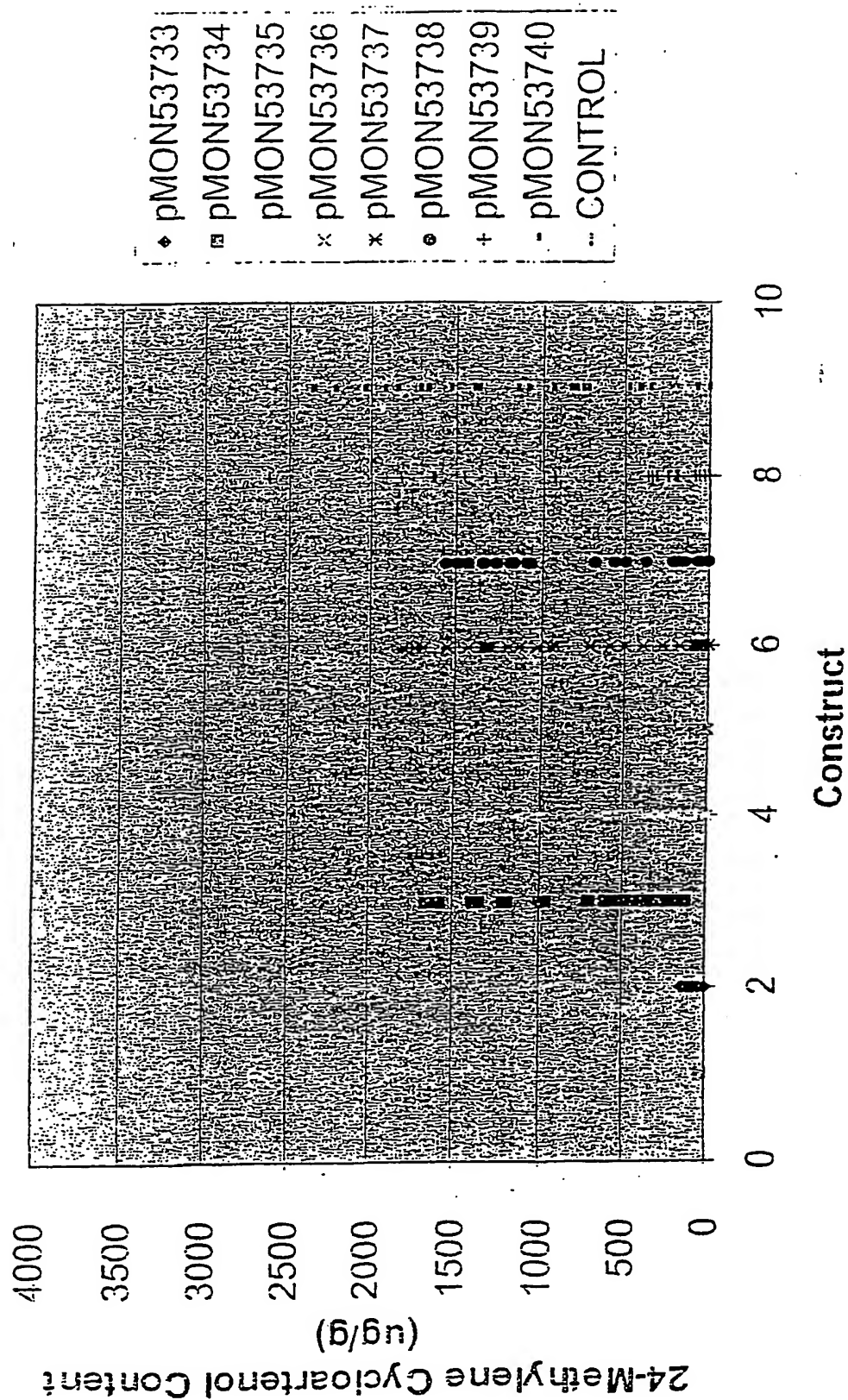


FIG. 23

Comparison of Obtusifolioside Levels in Transgenic Plants

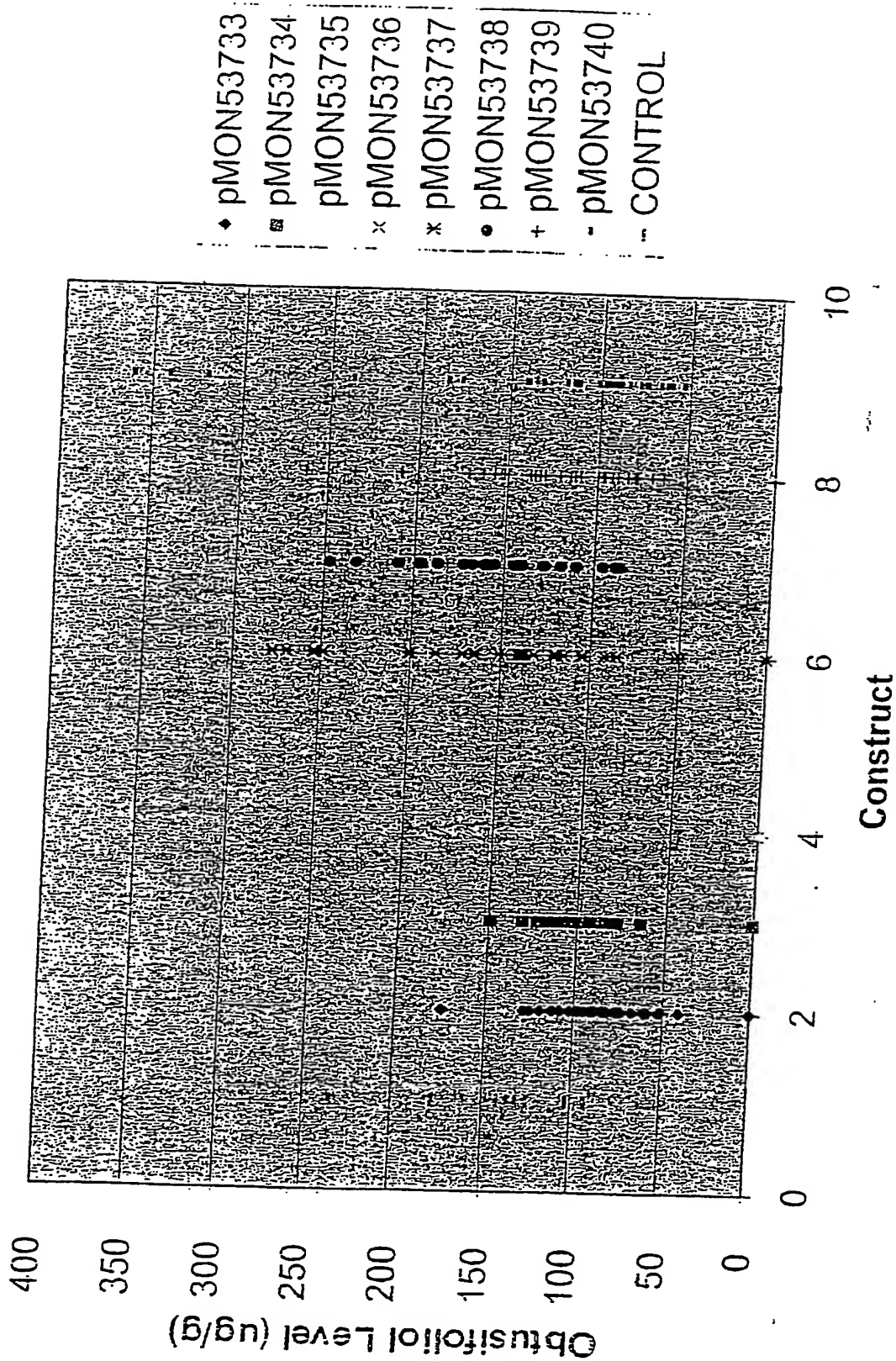


FIG. 24

Comparison of Campesterol Levels in Transgenic Plants

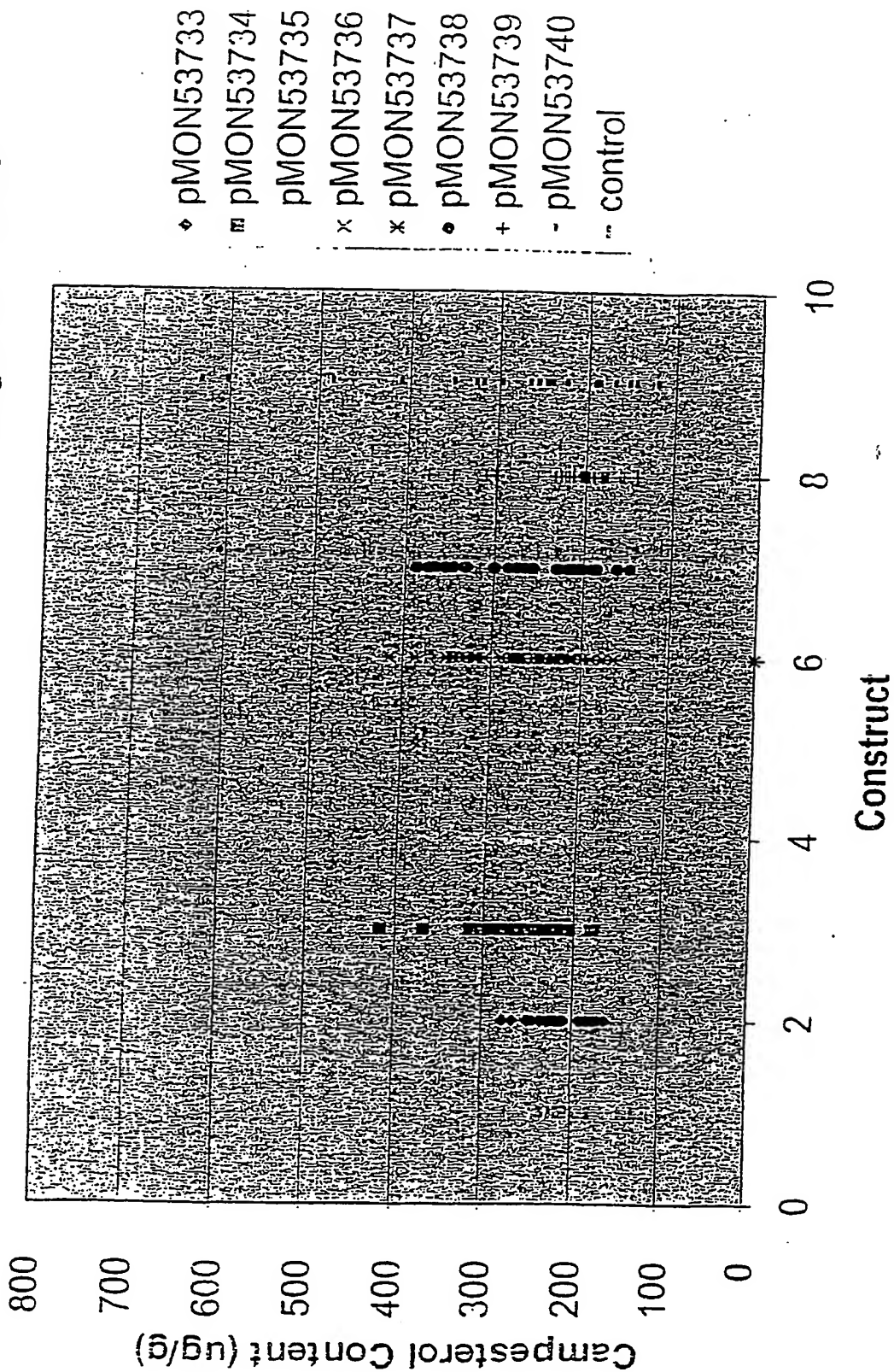


FIG. 25

Comparison of Sitosterol Levels in Transgenic Plants

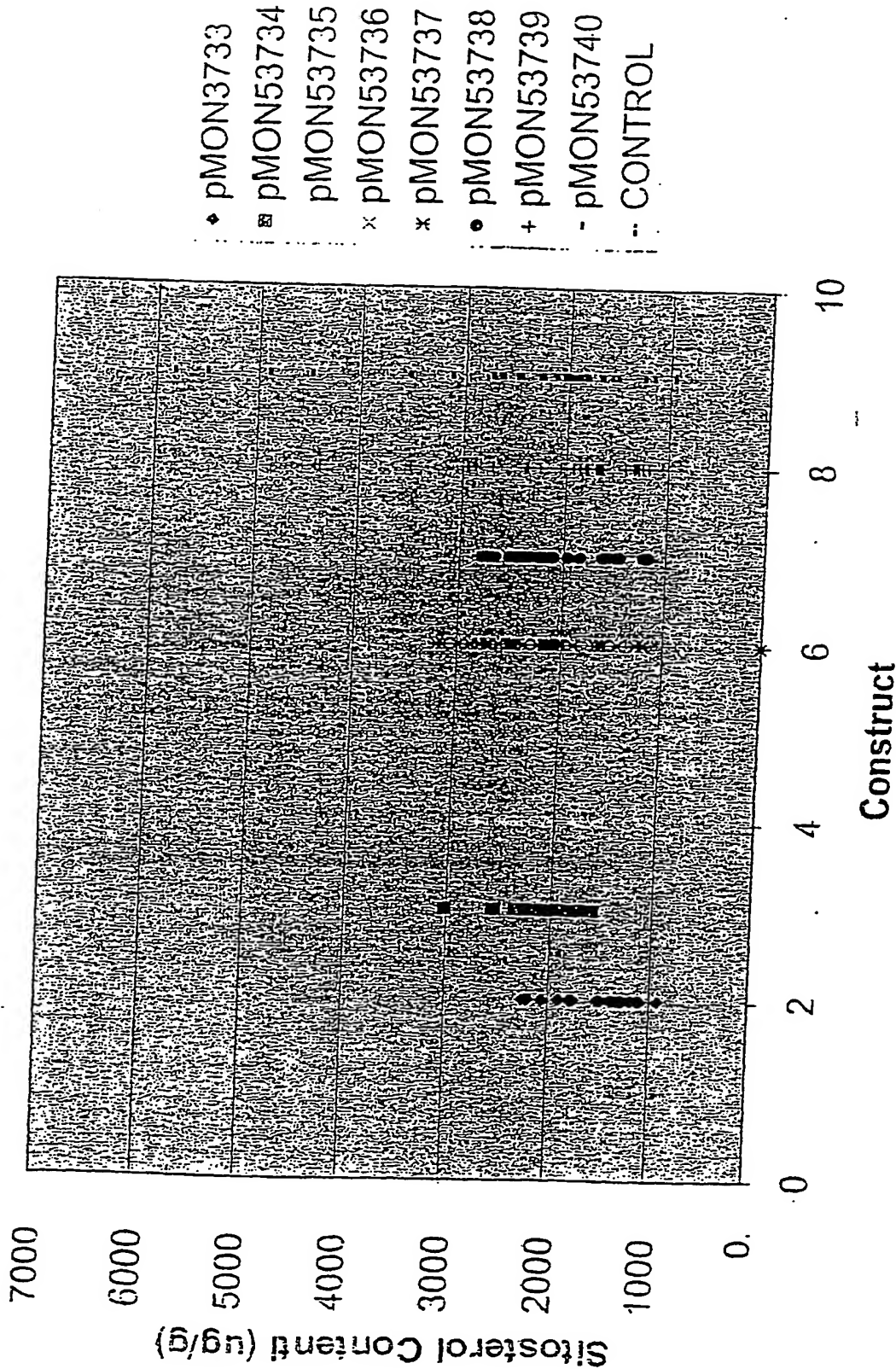


FIG. 26

Comparison of Sitostanol Levels in Transgenic Plants

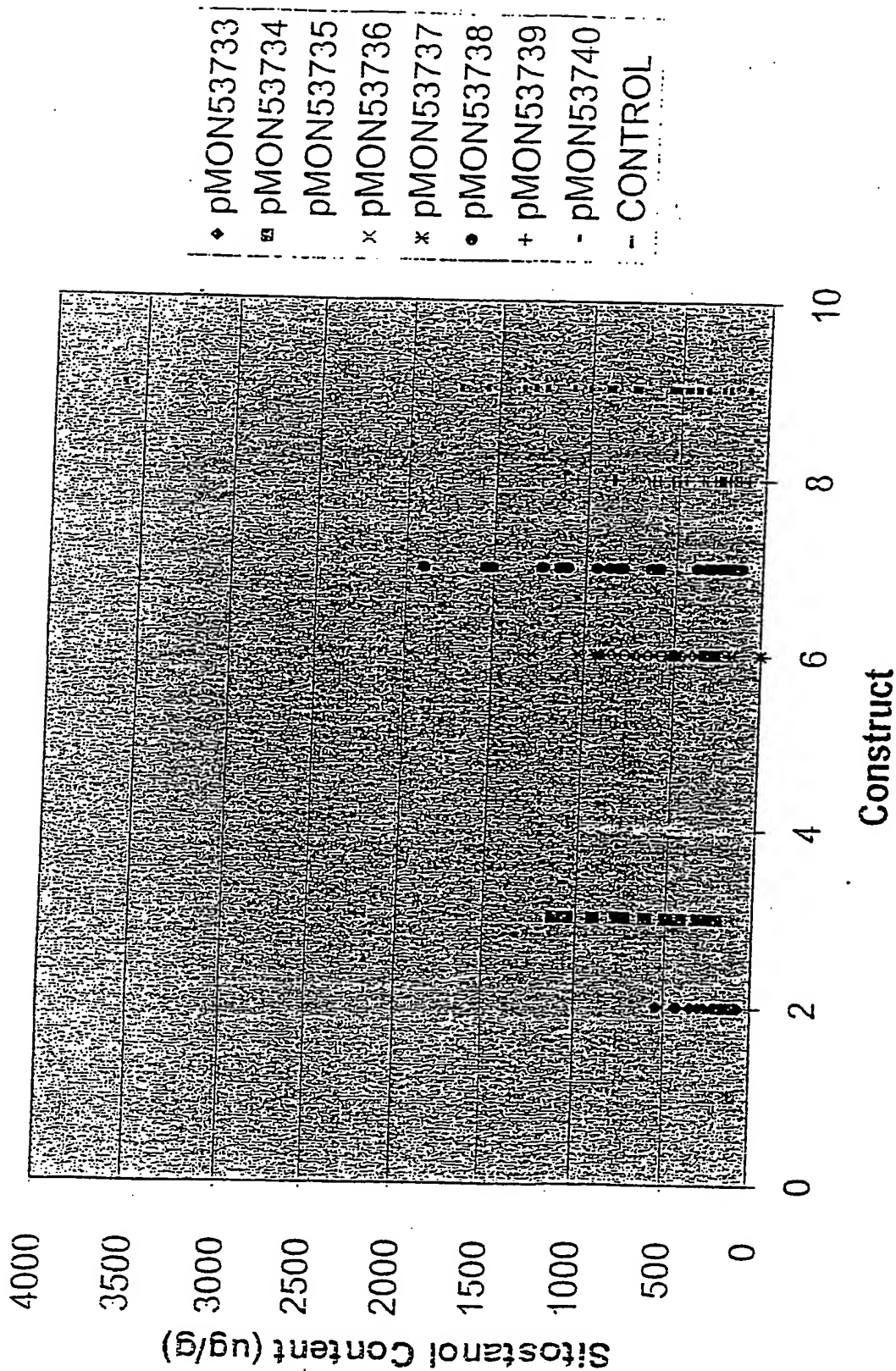


FIG. 27

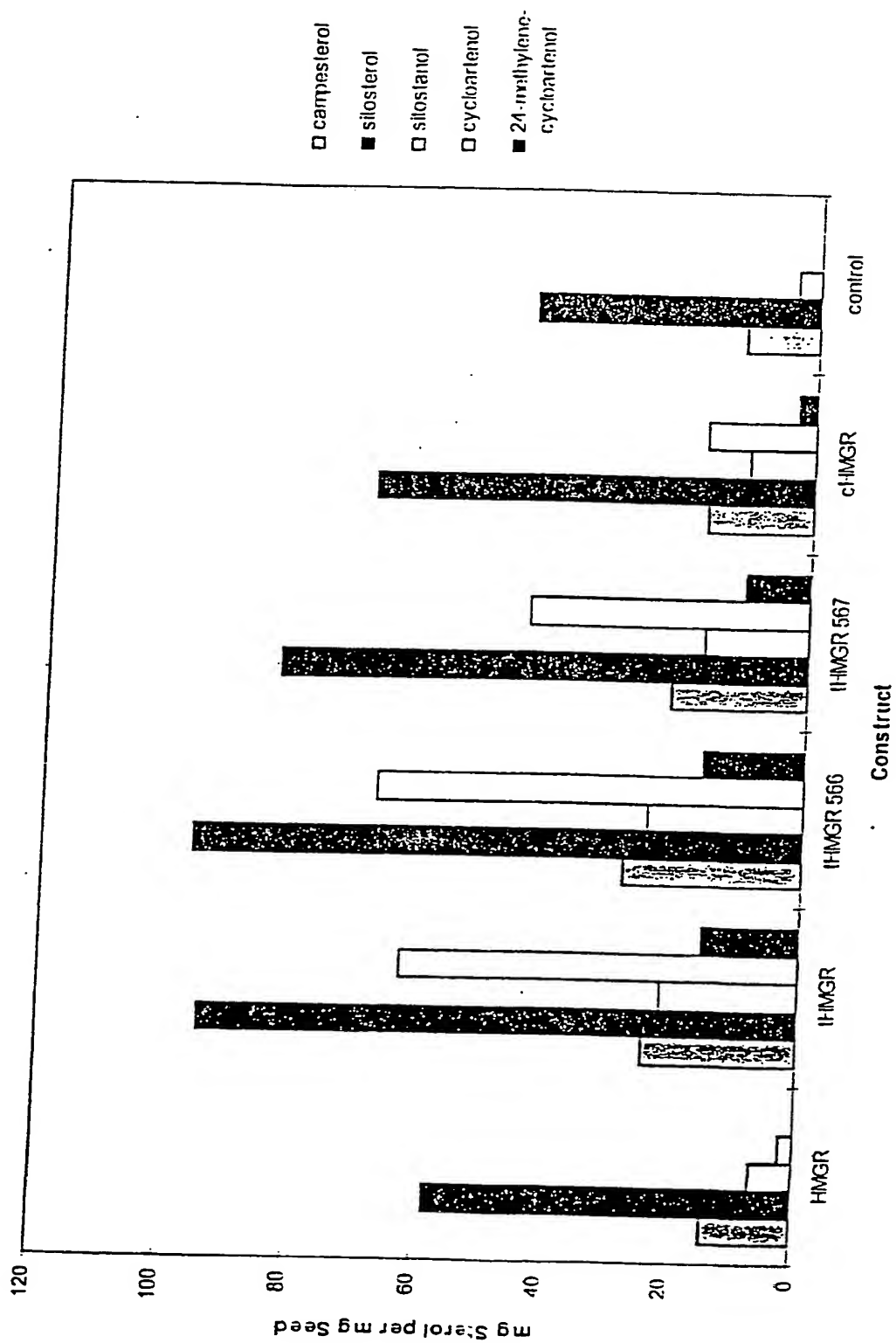
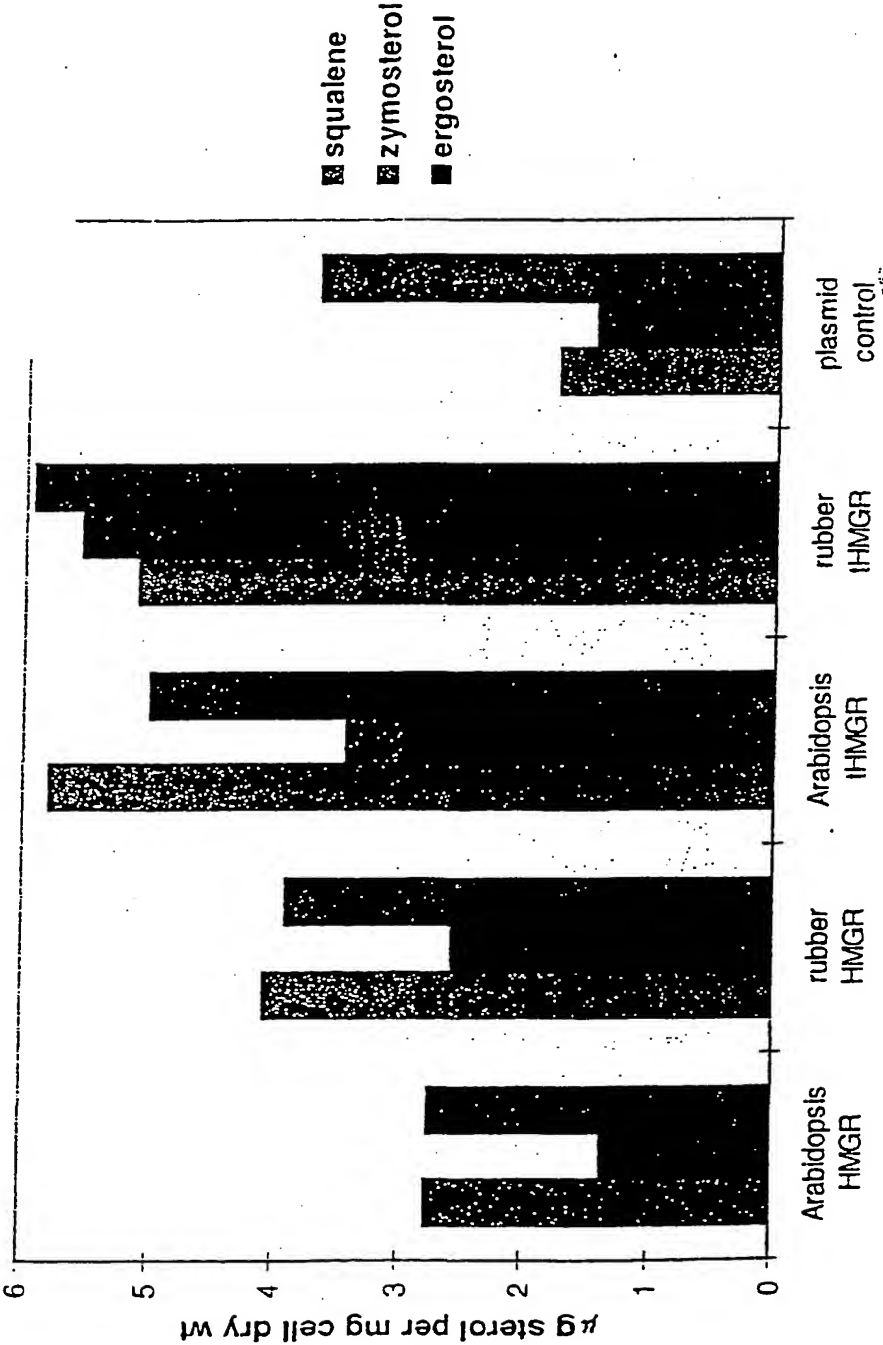


FIG. 28

Plant HMGR Constructs in Yeast HMGR1 Knockout Mutant



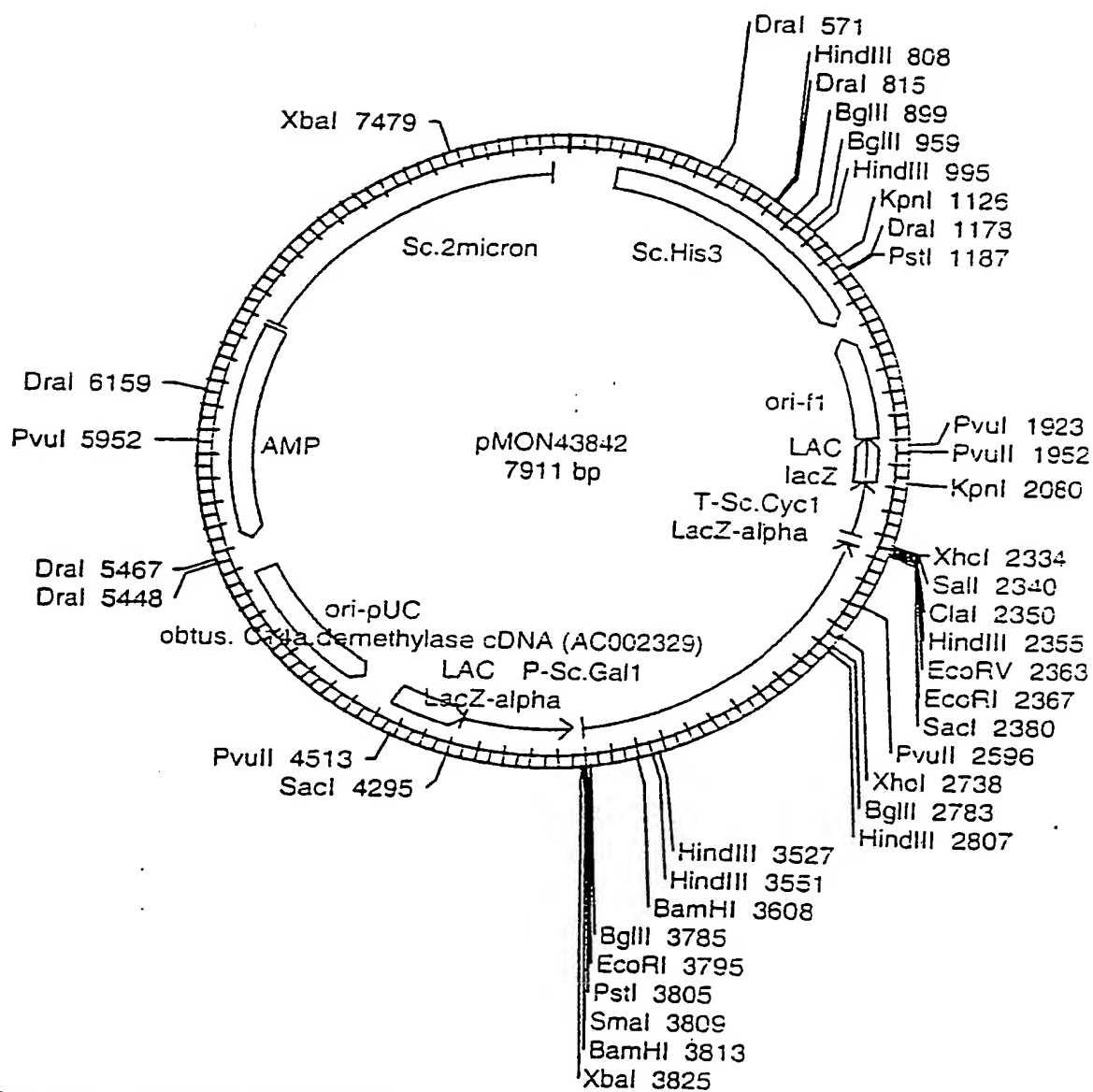


Figure 29: Construct pMON43842

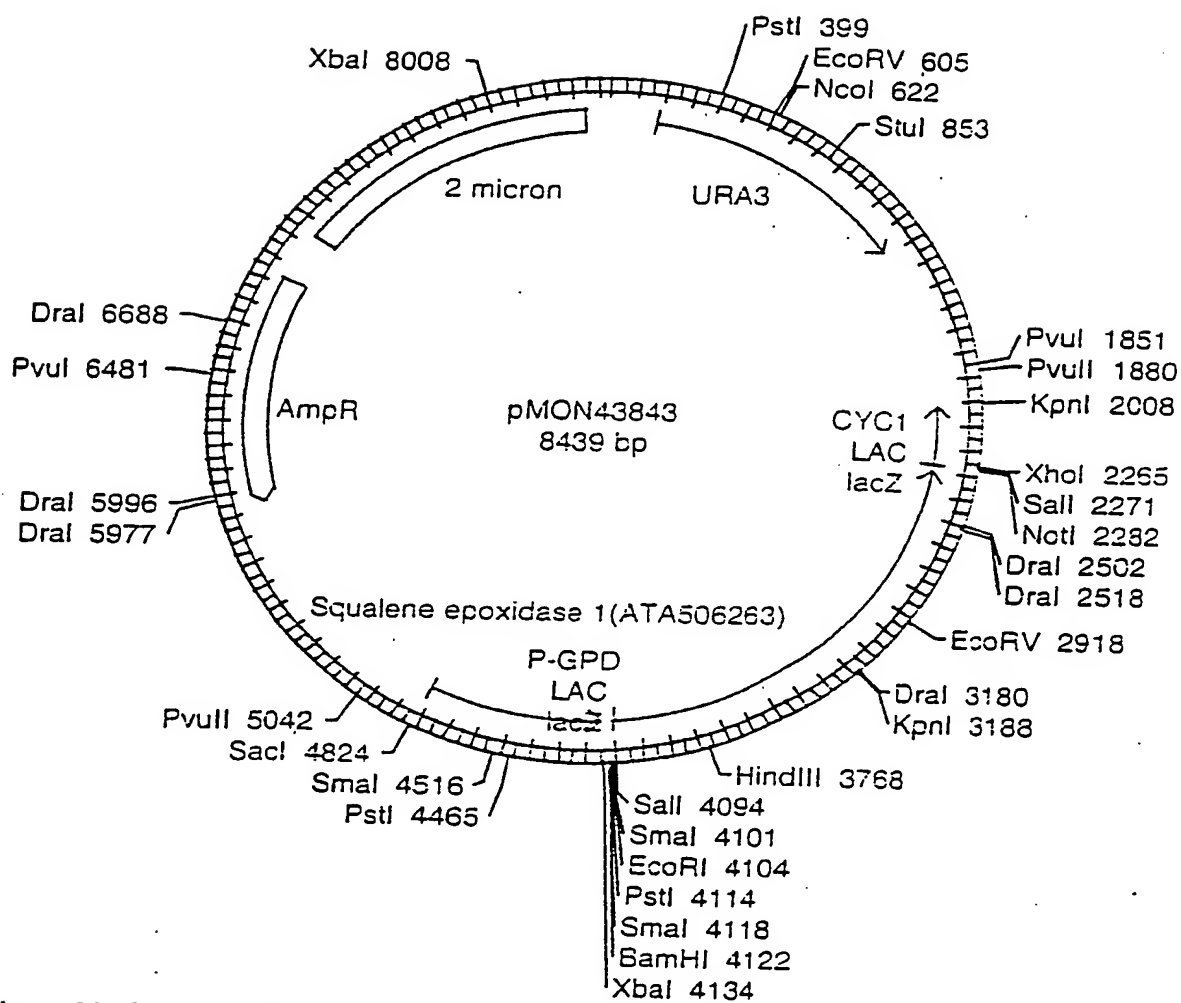


Figure 30: Construct pMON43843

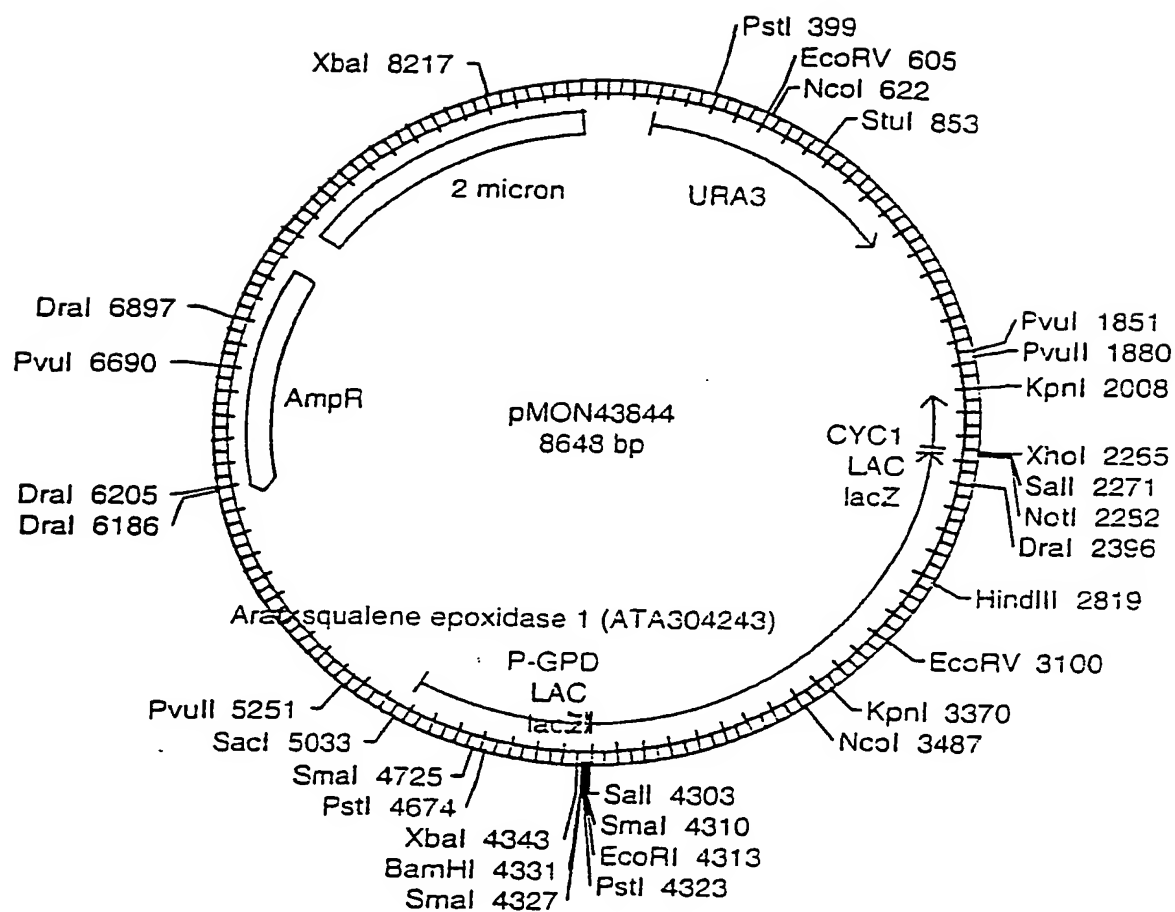


Figure 31: Construct pMON43844

FIG. 32A

Plurality: 5.00 Threshold: 4 AveWeight 1.00 AveMatch 2.91 AvMismatch -2.00
1

```

50
HMGRclustalW{methanobac} .....
.....
HMGRclustalW{methanococ} .....
.....
HMGRclustalW{halobacter} .....
.....
HMGRclustalW{sulfolobus} .....
.....
HMGRclustalW{      yeast2} MSLPLKTIVH LVKPFACAR FSARYPIEVI VVAVLLSAAA
YLSVTQSYLN
HMGRclustalW{      yeast1} MPPLFXGLKQ MAKPIAYVSR FSAKRPIHII LFSLIISAF
YLSVIQYYFN
HMGRclustalW{phycomyc} .....
.....
HMGRclustalW{  fusarium} .....
.....
HMGRclustalW{  candida} .....
.....
HMGRclustalW{dictyoste2} .....
.....
HMGRclustalW{wheat1} .....
.....
HMGRclustalW{      rice} .....
.....
HMGRclustalW{  corn} .....
.....
HMGRclustalW{wheat3} .....
.....
HMGRclustalW{wheat2} .....
.....
HMGRclustalW{      soybean} .....
.....
HMGRclustalW{rubbertre3} .....
.....
HMGRclustalW{rosyperiwi} .....
.....
HMGRclustalW{      tomato} .....
.....
HMGRclustalW{woodtobacc} .....
.....
HMGRclustalW{      potato} .....
.....
HMGRclustalW{radish} .....
.....
HMGRclustalW{arabadopsis1} .....
.....
HMGRclustalW{cucumismel} .....
.....
HMGRclustalW{rubbertre2} .....
.....
HMGRclustalW{rubbertre1} .....
.....
HMGRclustalW{camptothec} .....
.....
HMGRclustalW{arabadops2} .....
.....
HMGRclustalW{chineseham} .....
.....

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FIG. 32B

```
HMGRclustalW{chineseha2} .....
.....
HMGRclustalW{syrianhamst} .....
.....
HMGRclustalW{    rat} .....
.....
HMGRclustalW{    rabbit} .....
.....
HMGRclustalW{    human} .....
.....
HMGRclustalW{    mouse} .....
.....
HMGRclustalW{    xenopus} .....
.....
HMGRclustalW{sea urchin} .....
.....
HMGRclustalW{ cockroach} .....
.....
HMGRclustalW{drosophila} .....
.....
HMGRclustalW{dictyostel} .....
.....
HMGRclustalW{schistoscm} .....
.....
HMGRclustalW{archaecglo} .....
.....
HMGRclustalW{pseudomonas} .....
.....
-----
Consensus -----
```

FIG. 32C

	51
100	
HMGRclustalW(methanobac}
.....	
HMGRclustalW(methanococ}
.....	
HMGRclustalW(halobacter}
.....	
HMGRclustalW(sulfolobus}
.....	
HMGRclustalW(yeast2}	EWKLDNSN.QY STYLSIXPDE LFEKCTHYR SPVSDTWKLL
SSKEAADIYT	
HMGRclustalW(yeast1}	GWQLDSNSVF ETAPNKDSNT LFQECSHYR DSSLDGWVSI
TAHEASELPA	
HMGRclustalW(phycomyces}
.....	
HMGRclustalW(fusarium}MDH EGCQGQHPQQ
CCQWVSNAWS	
HMGRclustalW(candida}MFYH GASANQHWIA
VDDLKVPVD	
HMGRclustalW(dictyoste2}
.....	
HMGRclustalW(wheat1}
.....	
HMGRclustalW(rice}
.....	
HMGRclustalW(corn}
.....	
HMGRclustalW(wheat3}
.....	
HMGRclustalW(wheat2}
.....	
HMGRclustalW(soybean}
.....	
HMGRclustalW(rubbertre3}
.....	
HMGRclustalW(rosyperiwi}
.....	
HMGRclustalW(tomato}
.....	
HMGRclustalW(woodtobacc}
.....	
HMGRclustalW(potato}
.....	
HMGRclustalW(radish}
.....	
HMGRclustalW(arabadopsis1}
.....	
HMGRclustalW(cucumismel}
.....	
HMGRclustalW(rubbertre2}
.....	
HMGRclustalW(rubbertre1}
.....	
HMGRclustalW(camptothec}
.....	
HMGRclustalW(arabadops2}
.....	
HMGRclustalW(chineseham}MLSRLFRMH
GLFVASHPWE	
HMGRclustalW(chineseha2}MLSRLFRMH

FIG. 32D

```

GLFVASHPWE
  HMGRclustalW{syrianhamst} ..... .MLSRLFRMH
GLFVASHPWE
  HMGRclustalW{    rat} ..... .MLSRLFRMH
GLFVASHPWE
  HMGRclustalW{    rabbit} ..... .MLSRLFRMH
GLFVASHPWE
  HMGRclustalW{    human} ..... .MLSRLFRMH
GLFVASHPWE
  HMGRclustalW{    mouse} .....
.....
  HMGRclustalW{    xenopus} ..... .MLSRLFRMH
GQFVASHPWE
  HMGRclustalW{sea urchin} ..... .MLSRLFLAQ
GRFCSSHPWE
  HMGRclustalW{ cockroach} ..... .MVGRLFRAH
GQFCASHPWE
  HMGRclustalW{drosophila} ..... .MIGPLFRAT
.QFCASHPWE
  HMGRclustalW{dictyostel} .....
.....
  HMGRclustalW{schistosom} .....
.....
  HMGRclustalW{archaeoglo} .....
.....
  HMGRclustalW{pseudomonas} .....
.....
Consensus ----- -MLSRLFRMH
GLFVASHPWE

```


FIG. 32E

150	101
HMGRclustalW{methanobac}
.....
HMGRclustalW{methanococ}
.....
HMGRclustalW{halobacter}
.....
HMGRclustalW{sulfolobus}
.....
HMGRclustalW{ yeast2}	PFHYTLSTIS FQSKONSTTL PSLDDVIYSV DHTRYLLSEE
PKIPTELVSE	
HMGRclustalW{ yeast1}	PHEYLLNLN FNSPNETDSI PELANTVFEK DNTKYILQED
LSVSKEISST	
HMGRclustalW{phycomyces}
.....
HMGRclustalW{ fusarium}	EFLDLLKNAE TLDIVIMLLG YIAMHLTFVS LFLSMRKMGs
KFWLGICTLF	
HMGRclustalW{ candida}	VDHYNVVFFQ FRRAGEYKEP VLSGIVELDE VKFVVSQSDA
AEQWQQLTAE	
HMGRclustalW{dictyoste2}
.....
HMGRclustalW{wheat1}
.....
HMGRclustalW{ rice}
.....
HMGRclustalW{ corn}
.....
HMGRclustalW{wheat3}
.....
HMGRclustalW{wheat2}
.....
HMGRclustalW{ soybean}
.....
HMGRclustalW{rubbertre3}
.....
HMGRclustalW{rosyperiwi}
.....
HMGRclustalW{ tomato}
.....
HMGRclustalW{woodtobacc}
.....
HMGRclustalW{ potato}
.....
HMGRclustalW{radish}
.....
HMGRclustalW{arabadopsis1}
.....
HMGRclustalW{cucumismel}
.....
HMGRclustalW{rubbertre2}
.....
HMGRclustalW{rubbertre1}
.....
HMGRclustalW{camptothec}
.....
HMGRclustalW{arabadops2}
.....
HMGRclustalW{chineseham}	VIVGTVT..L TICMMSMN.. MFTGNNK...
.....

FIG. 32F

```

HMGRclustalW(chineseha2} VIVGTVT..L TICMMSMN.. MFTGNNK...
.....
HMGRclustalW(syrianhamst} VIVGTVT..L TICMMSMN.. MFTGNNK...
.....
HMGRclustalW( rat} VIVGTVT..L TICMMSMN.. MFTGNNK...
.....
HMGRclustalW( rabbit} VIVGTVT..L TICMMSMN.. MFTGNDK...
.....
HMGRclustalW( human} VIVGTVT..L TICMMSMN.. MFTGNNK...
.....
HMGRclustalW( mouse} .....
.....
HMGRclustalW( xenopus} VIVGTVT..L TICMMSMN.. MFTGNDK...
.....
HMGRclustalW(sea urchin} VIVCTLT..L TICMLSMN.. YFTGLPR...
.....
HMGRclustalW( cockroach} VIVATLT..L TVCMLTVDQ. RPLGLP....
.....
HMGRclustalW(drosophila} VIVALLT..I TACMLNGGQE QYPGCEQRIG HSTASAAAAG
SGSGAGSGAS
HMGRclustalW(dictyostel} .....
.....
HMGRclustalW(schistosom} .....
.....
HMGRclustalW(archaeogic} .....
.....
HMGRclustalW(pseudomonas} .....
.....

Consensus VIVGTVT--L TICMMSMN-- MFTGNNK---

```

FIG. 32G

200	151
HMGRclustalW{methanobac}
.....
HMGRclustalW{methanococ}
.....
HMGRclustalW{halobacter}
.....
HMGRclustalW{sulfolobus}
.....
HMGRclustalW{ yeast2}	NGTKWRLRNN SNFILDLENI YRNMVKQFSN KTSEFDQFDL
FIILAAYLTL	
HMGRclustalW{ yeast1}	DGTKWRLRSD RKSLFDVKTL AYSLYDVFE NVTQADPFDV
LIMVTAYLMM	
HMGRclustalW{phycomyces}
.....
HMGRclustalW{ fusarium}	SSVFAFLFGL VVTTKLGVP I SVILLSEGLP FLVVTIGFEK
NIVLTRAVMS	
HMGRclustalW{ candida}	DGTVWRSRAY HGKLGKYS DM AVGAFNKVLN LVRGAETFDI
ALVTCAYIAM	
HMGRclustalW{dictyoste2}
.....
HMGRclustalW{wheat1}
.....
HMGRclustalW{ rice}
.....
HMGRclustalW{ corn}
.....
HMGRclustalW{wheat3}
.....
HMGRclustalW{wheat2}
.....
HMGRclustalW{ soybean}
.....
HMGRclustalW{rubbertre3}
.....
HMGRclustalW{rosyperiwi}
.....
HMGRclustalW{ tomato}
.....
HMGRclustalW{woodtobacc}
.....
HMGRclustalW{ potato}
.....
HMGRclustalW{radish}
.....
HMGRclustalW{arabadopsis1}
.....
HMGRclustalW{cucumismel}
.....
HMGRclustalW{rubbertre2}
.....
HMGRclustalW{rubbertrel}
.....
HMGRclustalW{camptothec}
.....
HMGRclustalW{arabadops2}
.....
HMGRclustalW{chineseham}I CGWNYEC.PK FEEDVLSSDI
IILTITRCIA	

FIG. 32H

```

      HMGRclustalW{chineseha2} .....I CGWNYEC.PK FEEDVLSSDI
IILTITRCIA
      HMGRclustalW{syrianhamst} .....I CGWNYEC.PK FEEDVLSSDI
IILTITRCIA
      HMGRclustalW{      rat} .....I CGWNYEC.PK FEEDVLSSDI
IILTITRCIA
      HMGRclustalW{      rabbit} .....I CGWNYEC.PK FEEDVLSSDI
IILTITRCIA
      HMGRclustalW{      human} .....I CGWNYEC.PK FEEDVLSSDI
IILTITRCIA
      HMGRclustalW{      mouse} .....
.....
      HMGRclustalW{      xenopus} .....I CGWNYAC.PK FEEDVLSSDI
IILTITRCIA
      HMGRclustalW{sea urchin} .....I CGWNYECAQ VKESSLSSDV
LVMCIMRTLA
      HMGRclustalW{cockroach} ..... PGWGHNC..I TLEEYNAADM
IVMTLIRCVA
      HMGRclustalW{drosophila} GTIPPSSMGG SATSSRHRPC HGWSQSC.DG LEAEYNAADV
ILMTIVRCTA
      HMGRclustalW{dictyostel} .....
.....
      HMGRclustalW{schistosom} .....M LKILNTVLLF FDCFSTGTFF
VLLIYLFTRL
      HMGRclustalW{archaeoglo} .....
.....
      HMGRclustalW{pseudomonas} .....
.....
Consensus -----I CGWNYEC-PK FEEDVLSSDI
IILTITRCIA

```

FIG. 32I

250	201
HMGRclustalW{methanobac}
.....
HMGRclustalW{methanococ}
.....
HMGRclustalW{halobacter}
.....
HMGRclustalW{sulfolobus}
.....
HMGRclustalW{ yeast2}	FYTLCCFLND MRKIGSKFWL SFSALSNSAC ALYLSLYTTH
SLLKKPASLL	
HMGRclustalW{ yeast1}	FYTIFGLFND MRKTGSNFWL SASTVVNSAS SLFLALYVTQ
CILGKEVSAL	
HMGRclustalW{phycomyces}
.....
HMGRclustalW{ fusarium}	HAIEHRIQA QNSKSGKRSR DGSTQNMIOY AVQAAIKEXG
FEIIRDYAIE	
HMGRclustalW{ candida}	FYTFLNLFAR MRAVGSKVWL GLSTLVSSFF AFLFALYITT
RVLDLSIPFL	
HMGRclustalW{dictyoste2}
.....
HMGRclustalW{wheat1}
.....
HMGRclustalW{ rice}
.....
HMGRclustalW{ corn}
.....
HMGRclustalW{wheat3}
.....
HMGRclustalW{wheat2}
.....
HMGRclustalW{ soybean}
.....
HMGRclustalW{rubbertre3}
.....
HMGRclustalW{rosyperiwil}
.....
HMGRclustalW{ tomato}
.....
HMGRclustalW{woodtobacc}
.....
HMGRclustalW{ potato}
.....
HMGRclustalW{radish}
.....
HMGRclustalW{arabadopsis1}
.....
HMGRclustalW{cucumismel}
.....
HMGRclustalW{rubbertre2}
.....
HMGRclustalW{rubbertrel}
.....
HMGRclustalW{camptothec}
.....
HMGRclustalW{arabadops2}
.....
HMGRclustalW{chineseham}	ILYIYFQFQN LRQLGSKYIL GIAGLFTIFS SFVFSTVVIH
.....

FIG. 32J

```

      HMGRclustalW{chineseha2}  ILYIYFQFQN LRQLGSKYIL GIAGLFTIFS SFVFSTVVIH
      .....
      HMGRclustalW{syrianhamst}  ILYIYFQFQN LRQLGSKYIL GIAGLFTIFS SFVFSTVVIH
      .....
      HMGRclustalW{      rat}    ILYIYFQFQN LRQLGSKYIL GIAGLFTIFS SFVFSTVVIH
      .....
      HMGRclustalW{      rabbit}  ILYIYFQFQN LRQLGSKYIL GIAGLFTIFS SFVFSTVVIH
      .....
      HMGRclustalW{      human}   ILYIYFQFQN LRQLGSKYIL GIAGLFTIFS SFVFSTVVIH
      .....
      HMGRclustalW{      mouse}   .....
      .....
      HMGRclustalW{      xenopus}  ILYIYFQFQN LRQLGSKYIL GIAGLFTIFS SFVFSTVVIH
      .....
      HMGRclustalW{sea urchin}    VAYLYLQFTK LRTTGSKYIL GIAGLFTIFS SFLFSSAVIH
      .....
      HMGRclustalW{cockroach}     VLYSYYQFCH LQKLGSKYIL GIAGLFTVFS SFVFSSSVIN
      .....
      HMGRclustalW{drosophila}     VLYCYQQFCS LHRLGSKYVL GIAGLFTVFS SFIFTTAAIK
      .....
      HMGRclustalW{dictyostel}     .....
      .....
      HMGRclustalW{schistosom}     RTHLLHFSSS NCHLDVIIYQ SPRAVIIFLVV FVYFIGVLTC
      KINDKILVHT
      HMGRclustalW{archaeoglo}     .....
      .....
      HMGRclustalW{pseudomonas}    .....
      .....

      Consensus  ILYIYFQFQN LRQLGSKYIL GIAGLFTIFS SFVFSTVVIH -----
      -----

```

FIG. 32K

300	251
HMGRclustalW{methanobac}
.....
HMGRclustalW{methanococ}
.....
HMGRclustalW{halobacter}
.....
HMGRclustalW{sulfolobus}
.....
HMGRclustalW{ yeast2}	SLVIGLPFIV VIIG.FKHKV RLAAFSLQKF HRISIDKKIT
VSNIIYEAMF	
HMGRclustalW{ yeast1}	TLFEGLPFIV VVVG.FKHKI KIAQYALEKF ERVGLSKRIT
TDEIVFESVS	
HMGRclustalW{phycomyces}
.....
HMGRclustalW{ fusarium}	IVILVIGAAS GVQGGLOQFC FLAAWTLF.F DFILLETFYT
AILSILKLRST	
HMGRclustalW{ candida}	SLSEGIPFFV AVVG.FNNKI LLAEK/LQ.N QLNAQSSKND
APTVLYQALR	
HMGRclustalW{dictyoste2}
.....
HMGRclustalW{wheat1}
.....
HMGRclustalW{ rice}
.....
HMGRclustalW{ corn}M EVRG..... .GVGQGSAAAR
.....HPPA	
HMGRclustalW{wheat3}
.....
HMGRclustalW{wheat2}
.....
HMGRclustalW{ soybean}
.....
HMGRclustalW{rubbertre3}M DEVERRRPP.K HIVRKDHGGE
VLNSFSHG..	
HMGRclustalW{rosyperiwi}M DSRRRSP... TVTAKAAAGE
LPLAPHEGQ.	
HMGRclustalW{ tomato}M DVRRRSZEPV YPSKVFAADE
KPLKPHKKQQ	
HMGRclustalW{woodtobacc}M DVRRRSXKPA YPTKEFAAGE
KPLKPHK...	
HMGRclustalW{ potato}M DVRRRPVKPL YTSKDASAG.
EPLKQQE...	
HMGRclustalW{radish}M DIRR..RPPK PPVNSN....
...RFLDNRS	
HMGRclustalW{arabadosis1}M DLRR..RPPK PPVTNNNNNSN
GSFRSYQPRT	
HMGRclustalW{cucumismel}M DRRRSLRPPR PNAVQDADAT
CTFRRDEQDA	
HMGRclustalW{rubbertre2}
.....
HMGRclustalW{rubbertre1}M DTTG..RLH.HR....
.....KHAT	
HMGRclustalW{camptothec}M DVRRRSINSI HQIPSVGGTA
PPMLKPKQPT	
HMGRclustalW{arabados2}M EDLRRRFPTK KNAGEISN..
.....
HMGRclustalW{chineseham}	FLDKELTGLN EALPFFLLLI DLSRASALAK FALSSNSQDE
VRENIARGMA	

FIG. 32L

HMGRclustalW{chineseha2}	FLDKELTGLN	EALPFFLLLI	DLSRASALAK	FALSSNSQDE
VRENIARGMA				
HMGRclustalW{syrianhamst}	FLDKELTGLN	EALPFFLLLI	DLSRASALAK	FALSSNSQDE
VRENIARGMA				
HMGRclustalW{rat}	FLDKELTGLN	EALPFFLLLI	DLSRASALAK	FALSSNSQDE
VRENIARGMA				
HMGRclustalW{rabbit}	FLDKELTGLN	EALPFFLLLI	DLSRASALAK	FALSSNSQDE
VRENIARGMA				
HMGRclustalW{human}	FLDKELTGLN	EALPFFLLLI	DLSRASTLAK	FALSSNSQDE
VRENIARGMA				
HMGRclustalW{mouse}
.....				
HMGRclustalW{xenopus}	FLDKELTGLN	EALPFFLLLI	DLSKASALAK	FALSSNSQDE
VRDNIARGMA				
HMGRclustalW{sea urchin}	LFGLELTGLN	EALPFFLLLI	DLTKASALTK	FALSSTTQNE
VVDNIARGMA				
HMGRclustalW{cockroach}	FLGSDVSDLK	DALFFFLLLI	DLSKATVLAQ	FALSSRSQDE
VKHNIARGIA				
HMGRclustalW{drosophila}	FLGSDISELK	DALFFLLLLVI	DLSNSGRLRS	GAMGSN.QAE
VTQNIARGLE				
HMGRclustalW{dictyostel}
.....				
HMGRclustalW{schistosom}	MLRNKRQLNT	LFYTLILFTF	ALCSLSSVLF	VPYTSFAIFL
LSTSVFLLFS				
HMGRclustalW{archaeoglo}
.....				
HMGRclustalW{pseudomonas}
.....				
	Consensus	FLDKELTGLN	EALPFFLLL-	DL-RASALAK FALSSNSQDE
VRENIARGMA				

FIG. 32M

350	HMGRclustalW{methanobac}	301
.....	HMGRclustalW{methanococ}	
.....	HMGRclustalW{halobacter}	
.....	HMGRclustalW{sulfolobus}	
.....	HMGRclustalW{ yeast2}	QEGAYLIRDY LFYISSFIGC AIYARHLPGL VNFCILSTFM	
LVFDLLLSAT	HMGRclustalW{ yeast1}	EEGGRLIQDH LLCIFAFIGC SMYAHQLKTL TNFCILSAFI	
LIFELILTPT	HMGRclustalW{phycomyces}	
.....	HMGRclustalW{ fusarium}	VSSVMSICVW PLRMMASRRV AENVAKGDEE LNRVRGDAPL	
FGRKSSSIPK	HMGRclustalW{ candida}	EQGPLLLRDE LFMITAFLGC SFYASYLDGL KNFCILAALI	
LAFDILTST	HMGRclustalW{dictyoste2}	
.....	HMGRclustalW{wheat1}	
.....	HMGRclustalW{ rice}MRIT.....	
...NGLAMVS	HMGRclustalW{ corn}	PE....PSRAAA RVQAGDALPL PIRHT.....	
...NLIFSAL	HMGRclustalW{wheat3}	
.....	HMGRclustalW{wheat2}	
.....	HMGRclustalW{ soybean}	
.....	HMGRclustalW{rubbertre3}HH L.....PP LKPSDYSLPL SLYLA.....	
...NALVFSL	HMGRclustalW{rosyperiwi}NQ Q.....PS IPRSSDVLPL PLYLA.....	
...NGVFFTL	HMGRclustalW{ tomato}	QQ....QEDK N.....TL LIDASDALPL PLYLTT....	
...NGLFFTM	HMGRclustalW{woodtobacc}	QQ....QECD N.....SL LI.ASDALPL PLYLT.....	
...NGLFFTM	HMGRclustalW{ potato}VS SPKASDALPL PLYLT.....	
...NGLFFTM	HMGRclustalW{radish}	DD....DDRR K.....TLTS PPKASDALPL PLYLT.....	
...NAVFFTL	HMGRclustalW{arabadosis1}	SD....DDER RR..ATTIAP PPKASDALPL PLYLT.....	
...NAVFFTL	HMGRclustalW{cucumismel}	SA....ADHL KR.....A SPKASDALPL PLYLT.....	
...NTIFFTL	HMGRclustalW{rubbertre2}	
.....	HMGRclustalW{rubbertre1}	PV....EDRS P.....T TPKASDALPL PLYLT.....	
...NAVFFTL	HMGRclustalW{camptothec}	KV....DAVD L.....PD SPKASDALPL PLYIT.....	
...NGVFFTL	HMGRclustalW{arabados2}VAVDPP LRKASDALPL PLYLT.....	
...NTFFLSL	HMGRclustalW{chineseham}	ILGPTFTLDA LV..ECLVIG VGTMSGVRQL EIMCCFGCMS	
VLANYFVFMT			

FIG. 32N

HMGRclustalW(chineseha2)	ILGPTFTLDA LV..ECLVIG VGTMSGVRQL EIMCCFGCMS
VLANYFVFMT	
HMGRclustalW(syrianhamst)	ILGPTFTLDA LV..ECLVIG VGTMSGVRQL EIMCCFGCMS
VLANYFVFMT	
HMGRclustalW(rat)	ILGPTFTLDA LV..ECLVIG VGTMSGVRQL EIMCCFGCMS
VLANYFVFMT	
HMGRclustalW(rabbit)	ILGPTFTLDA LV..ECLVIG VGTMSGVRQL EIMCCFGCMS
VLANYFVFMT	
HMGRclustalW(human)	ILGPTFTLDA LV..ECLVIG VGTMSGVRQL EIMCCFGCMS
VLANYFVFMT	
HMGRclustalW(mouse)
.....	
HMGRclustalW(xenopus)	ILGPTFTLEA LV..ECLVIG VGTMSGVRQL EIMCCFGCMS
VLANYFAFMT	
HMGRclustalW(sea urchin)	ILGPTITLDT VV..TTLVIS IGTSSIRKM EVFCCFGILS
LIANYFVFMT	
HMGRclustalW(cockroach)	MLGPTITLDT VV..ETLVIG VGMLSGVRRL EVLCCFACMS
VIVNYVVFMT	
HMGRclustalW(drosophila)	LLGPAISLDT IV..VLLVG VGTLSGVQRL EVLCMFAVLS
VLVNYVVFMT	
HMGRclustalW(dictyostel)M LFAPPNLETK ELFWIYY.IL
ILIPKVFAKV	
HMGRclustalW(schistosom)	DLSVFFIVLE YYLLEIELVN YEHAKRCLL SHLFSNQLFV
DEMLGMFLKT	
HMGRclustalW(archaeoglo)
.....	
HMGRclustalW(pseudomonas)
.....	
Consensus	ILGPTFTLDA LV--ECLVIG VGTASD-LPL -LYCTFGCMS
VLANYFFFMT	

FIG. 320

400
 HMGRclustalW{methanobac}

 HMGRclustalW{methanococ}

 HMGRclustalW{halobacter}

 HMGRclustalW{sulfolobus}

 HMGRclustalW{ yeast2} FYSAILSMKL EINIIHRSTV IRQTL..EED GVVPTTADII
 YKDETASEPH
 HMGRclustalW{ yeast1} FYSAILALRL EMNVIHRSTI IKQTL..EED GVVPTSTARI
 SKAEKKS SVSS
 HMGRclustalW{phycomyces}

 HMGRclustalW{ fusarium} FKVLMILGFI FVNIVNICSI PFRNP..SSM STIRTWASSL
 GGVIAPLSVD
 HMGRclustalW{ candida} FLSAILSLKL EINQIHRSTL LREQ..EDD GLTETTVDVV
 LKSNLSLAGTK
 HMGRclustalW{dictyoste2}

 HMGRclustalW{wheat1}

 HMGRclustalW{ rice} LVLSSCDLVR LCSDRER... PL.....GGREFA
 TVVCQLASVV
 HMGRclustalW{ corn} FAASLAYLMR RWREKIRSST PLHA.....VGLAEML
 AIFGLVASLI
 HMGRclustalW{wheat3}

 HMGRclustalW{wheat2}

 HMGRclustalW{ soybean}

 HMGRclustalW{rubbertre3} FFSVAYFLLH RWREKIRKST PLHI.....VTFPEIA
 ALICLVASVI
 HMGRclustalW{rosyperiwi} FFSVMYFLLT RWREKIRNAT PLHV.....VTLSELA
 ALASLIASVI
 HMGRclustalW{ tomato} FFSVMYFLLS RWREKIRNST PLHV.....VTLSELG
 AIVSLIASVI
 HMGRclustalW{woodtobacc} FFSVMYFLLS RWREKIRNST PLHV.....VTFSELV
 AIASLIASVI
 HMGRclustalW{ potato} FFSVMYFLLV RWREKIRNSI PLHV.....VTLSELL
 AMVSLIASVI
 HMGRclustalW{radish} FFSVAYYLLH RWRDKIRYNT PLHV.....VTVTELG
 AIVALIASFI
 HMGRclustalW{arabadosis1} FFSVAYYLLH RWRDKIRYNT PLHV.....VTITELG
 AIIALIASFI
 HMGRclustalW{cucumismel} FFSVAYYLLH RWRDKIRNST PLHV.....VTLSEIA
 AIVSLMASFI
 HMGRclustalW{rubbertre2}

 HMGRclustalW{rubbertrel} FFSVAYYLLH RWRDKIRNST PLHI.....VTLSEIV
 AIVSLIASFI
 HMGRclustalW{camptothec} FFTVVYLLV RWREKIRNST PLHV.....VTLSEIA
 AIFTFVASFI
 HMGRclustalW{arabados2} FFTATVYLLS RWREKIRNST PLHV.....VDLSEIC
 ALIGFVASFI
 HMGRclustalW{chineseham} FFPACVSLVL ELSRESREGR PIWQ...LSH FARVLEEEZ.
 NKPNPVTQRV

FIG. 32P

HMGRclustalW{chineseha2}	FFPACVSLVL ELSRESREGR PIWQ...LSH FARVLEEEEE.
NKPNPVTQRV	
HMGRclustalW{syrianhamst}	FFPACVSLVL ELSRESREGR PIWQ...LSH FARVLEEEEE.
NKPNPVTQRV	
HMGRclustalW{ rat}	FFPACVSLVL ELSRESREGR PIWQ...LSH FARVLEEEEE.
NKPNPVTQRV	
HMGRclustalW{ rabbit}	FFPACVSLVL ELSRESREGR PIWQ...LSH FARVLEEEEE.
NKPNPVTQRV	
HMGRclustalW{ human}	FFPACVSLVL ELSRESREGR PIWQ...LSH FARVLEEEEE.
NKPNPVTQRV	
HMGRclustalW{ mouse}
.....	
HMGRclustalW{ xenopus}	FFPACVSLVL ELSRESREGR PIWQ...LSQ FASVLEEEEE.
NKPNPVTQRV	
HMGRclustalW{sea urchin}	FFPACLSLVL ELSNSNKYGR PVWH...LGR FAEVLEEEEE.
RKPNPVVQRV	
HMGRclustalW{ cockroach}	FYPACLSLIL.ELSRSGESGR PAWHD..KSL IIKALHEED.
QKPNPVVQRV	
HMGRclustalW{drosophila}	FYPACLSLIF DLSRSGVDMS VVREKAKGSL PLKSLTEEE.
QKPNPVLQRV	
HMGRclustalW{dictyostel}	MSVRELFPFF KWGFNIRRSN FLVP..... ILSNNVI
VTGEEAVQYE	
HMGRclustalW{schistosom}	SLFSISTTSK YAYLESIFKC TLMEQIIYIM IVFVFLPSFM
RIFASYAKRM	
HMGRclustalW{archaeoglo}
.....	
HMGRclustalW{pseudomonas}
.....	
Consensus	FFSACYSLLL -WRRKIRNST PLHV---LSH FARVTLEEEA AXPN-
VASRI	

FIG. 32Q

	401	
450		
HMGRclustalW{methanobac}	
.....		
HMGRclustalW{methanococ}	
.....		
HMGRclustalW{halobacter}	
.....		
HMGRclustalW{sulfolobus}	
.....		
HMGRclustalW{ yeast2}	FLRSNVAILL GKASVIGLLL LINLYVF... .TDKLNATIL	
NTVYFDSTIY		
HMGRclustalW{ yeast1}	FLNLSVVVII MKLSVILLFV FINFYNF... GANWVN.DAF	
NSLYFDKERV		
HMGRclustalW{phycomyces}	
.....		
HMGRclustalW{ fusarium}	PFKVASNGLD AILFTAKSNN RPTLVTV... LTPIKYELEY	
PSIHIALGSA		
HMGRclustalW{ candida}	TFTDAPSTLV TVAKVAGVSV FFGLHIFY... GFGSAWLSDL	
SAGNETNDTF		
HMGRclustalW{dictyoste2}	
.....		
HMGRclustalW{wheat1}	
.....		
HMGRclustalW{ rice}	YLLSLFAHPD APATTGDDD	
.....		
HMGRclustalW{ corn}	YLLSFFGIAF VQSIVSSGDD	
.....		
HMGRclustalW{wheat3}	
.....		
HMGRclustalW{wheat2}	
.....		
HMGRclustalW{ soybean}	
.....		
HMGRclustalW{rubbertre3}	YLLGFFGIGF VHSFS.RAST	
.....		
HMGRclustalW{rosyperiwi}	YLVSFFGLDF VQSLIYKPNN	
.....		
HMGRclustalW{ tomato}	YLLGFFGIGF VQTFVSRGNN	
.....		
HMGRclustalW{woodtobacc}	YLLGFFGIGF VQSFVSRDNN	
.....		
HMGRclustalW{ potato}	YLLGFFGIGF VQSFVSRSNS	
.....		
HMGRclustalW{radish}	YLLGFFGIDF VQSFISRP..	
.....		
HMGRclustalW{arabadosis1}	YLLGFFGIDF VQSFISRASG	
.....		
HMGRclustalW{cucumismel}	YLLGFFGIDF VQSFIRSSP	
.....		
HMGRclustalW{rubbertre2}	
.....		
HMGRclustalW{rubbertre1}	YLLGFFGIDF VQSFIRASH	
.....		
HMGRclustalW{camptothec}	YLLGFFGIGL VQPFTSRSSH	
.....		
HMGRclustalW{arabados2}	YLLGFCGIDL IFRSS..SD.	
.....		
HMGRclustalW{chineseham}	KMIMSLGLVL VEAHSRWIAD PSPQNST... TE.HSKVSLG	
LDDEVSKRIE		

FIG. 32R

HMGRclustalW{chineseha2}	KMIMSLGLVL	VHAHSRWIAD	PSPQNST...	TE.HSKVSLG
LDEDVSKRIE				
HMGRclustalW{syrianhamst}	KMIMSLGLVL	VHAHSRWIAD	PSPQNST...	TE.HSKVSLG
LDEDVSKRIE				
HMGRclustalW{rat}	KMIMSLGLVL	VHAHSRWIAD	PSPQNST...	AE.QSKVSLG
LAEDVSKRIE				
HMGRclustalW{rabbit}	KMIMSLGLVL	VHAHSRWIAD	PSPQNST...	AD.NSKVSLG
LDENVSKRIE				
HMGRclustalW{human}	KMIMSLGLVL	VHAHSRWIAD	PSPQNST...	AD.TSKVSLG
LDENVSKRIE				
HMGRclustalW{mouse}
.....				
HMGRclustalW{xenopus}	KMIMSLGLVL	VHAESRWISE	PSSQNST...	SISDHEVTTM
LDDMMPKRVE				
HMGRclustalW{sea urchin}	KMIMRTGLVL	VHAHSYWLASNDT...	ELMSRDMLYD
GNLLTDKKID				
HMGRclustalW{cockroach}	KVIMSAGLML	VHAH.RWVRCL.
.....				
HMGRclustalW{drosophila}	KLIMTTGLMA	VHIYSREVS?AAT...	TMVDKTLTPT
LSLNVSNNRT				
HMGRclustalW{dictyostel}	KPLPYIPQHN	QQQQQKQQPS
.....				
HMGRclustalW{schistosom}	YGEQKCLVS	NXGVSSSTRK	RRHSYSSGHS	YVEYRRMSVH
NLIGYVNP				
HMGRclustalW{archaeoglo}
.....				
HMGRclustalW{pseudomonas}
.....				
	Consensus	YLL-FFG-VL	V-A-SR-ISD	PSPQNST--- ----SKVSLG LDE-
VSKRIE				

FIG. 32S

500	451
HMGRclustalW{methanobac}
.....
HMGRclustalW{methanococ}
.....
HMGRclustalW{halobacter}
.....
HMGRclustalW{sulfolobus}
.....
HMGRclustalW{ yeast2}	SLPNFINYKD IGNLSNQVII SVLPKQYYTP LKKYHQIEDS
VLLIIDSVS	
HMGRclustalW{ yeast1}	SLPDFITSNA SENFKEQAIV SVTPLLYYKP IKSQRIEDM
VLLLLLRNVSV	
HMGRclustalW{phycomyces}
.....
HMGRclustalW{ fusarium}	ASNPAYN.DA FHHHFQGYGV GGRMVGGILK SLEDPVLSKN
IVIALALSVA	
HMGRclustalW{ candida}	TLYDAVA.DQ IPIGSNGTLV TLFPTRFLLP EXLSTQIEAV
VLSFIGLIST	
HMGRclustalW{dictyoste2}
.....
HMGRclustalW{wheat1}
.....
HMGRclustalW{ rice}	..D.....
.....
HMGRclustalW{ corn}	..DEDFLVGS G.....
.....
HMGRclustalW{wheat3}
.....
HMGRclustalW{wheat2}
.....
HMGRclustalW{ soybean}
.....
HMGRclustalW{rubbertre3}	..D.SWDVEE Y.....D DDNIIIKEDT
R.....	
HMGRclustalW{rosyperiwi}	..E.GWEIEEEILMVEDS
RN.....	
HMGRclustalW{ tomato}	..D.SWDE..N DEEFLLKEDS
RC.....	
HMGRclustalW{woodtobacc}	..DECWDEED E.....N DEQFLLEEDS
RR.....	
HMGRclustalW{ potato}	..D.SWDIED E.....N AEQLIIEEDS
RR.....	
HMGRclustalW{radish}	..D.SGDSE R.....DFDDH
R.....	
HMGRclustalW{arabadosis1}	..D.AWDLAD T.....IDDDDH
R.....	
HMGRclustalW{cucumismel}	..D.AWDLADEIDRT
L.....	
HMGRclustalW{rubbertre2}
.....
HMGRclustalW{rubbertre1}	..D.VWDLED T.....D P.NYLIDEDH
R.....	
HMGRclustalW{camptothec}	..DDVWGVD DE.....D VDEIVLKEDT
R.....	
HMGRclustalW{arabados2}	..DDVWVNDGD
.....	
HMGRclustalW{chineseham}	PSVSLWQFYL SKMISMDIEQ VVTLSLAFLL AVKYIFFEQA
ET..ESTLSL	

FIG. 32T

```

      HMGRclustalW{chineseha2} PSVSLWQFYL SKMISMDIEQ VVTLSLAFLLL AVKYIFFEQA
ET..ESTLSL
      HMGRclustalW{syrianhamst} PSVSLWQFYL SKMISMDIEQ VVTLSLAFLLL AVKYIFFEQA
ET..ESTLSL
      HMGRclustalW{      rat} PSVSLWQFYL SKMISMDIEQ VITLSLALLL AVKYIFFEQA
ET..ESTLSL
      HMGRclustalW{      rabbit} PSVSLWQFYL SKMISMDIEQ VITLSLALLL AVKYIFFEQA
ET..ESTLSL
      HMGRclustalW{      human} PSVSLWQFYL SKMISMDIEQ VITLSLALLL AVKYIFFEQT
ET..ESTLSL
      HMGRclustalW{      mouse} .....
.....
      HMGRclustalW{      xenopus} PSMPWLWQFYL SRMVTMDVEQ IITLGLALLL AVKYIFFEQT
ET..ESTFSM
      HMGRclustalW{sea urchin} PTMPLWEFYA TRLWPPTLDY ILTAILATVL ASHYIFFSDL
ATYPEKRVSI
      HMGRclustalW{cockroach} .SIALWPDLT S.....LRY FCTHCDTGVS YSRWSFASEG
EE..LPTVKL
      HMGRclustalW{drosophila} ESGEIADIII KWL.TMSADH IVISIVLIAL VVKFICFDNR
DP...LPDQL
      HMGRclustalW{dictyostel} ..QDYIQQPQ ..... ..N....DNN
IN.....
      HMGRclustalW{schistoscm} CHYKCWSTTF VIFVSLIILH LNNRYSERIS SFKNSSENE
VFPVLYHITA
      HMGRclustalW{archaeoglo} .....
.....
      HMGRclustalW{pseudomonas} .....
.....

Consensus PSDSLWDFY- SKMISMDIEQ VVTLSLA-LL AVKYIFFED- RT--
ESTLSL

```


FIG. 32U

550	501
HMGRclustalW{methanobac}
.....
HMGRclustalW{methanococ}
.....
HMGRclustalW{halobacter}
.....
HMGRclustalW{sulfolobus}
.....
HMGRclustalW{ yeast2}	AIRDQFISKL LFFAFAVSIS INVYLLNAAK IHTGYMNFQ.
..PQSNKIDD	
HMGRclustalW{ yeast1}	AIRDQFVSKL VLSALVCSAV INVYLLNAAK IHTSYTADQL
VKTEVTKKSF	
HMGRclustalW{phycomyces}
.....
HMGRclustalW{ fusarium}	LNGYLFNVAR WGIKDPNVPE HNIDRNELAR AREFNDTGS.
.....AT	
HMGRclustalW{ candida}	AARDKYISKF ILFAFAVSAS INVYLLNVAR IHTTRLEDA.
.....IE	
HMGRclustalW{dictyoste2}
.....
HMGRclustalW{wheat1}
.....
HMGRclustalW{ rice}
.....
HMGRclustalW{ corn}
.....
HMGRclustalW{wheat3}
.....
HMGRclustalW{wheat2}
.....
HMGRclustalW{ soybean}
.....
HMGRclustalW{rubbertre3}
.....G.....
HMGRclustalW{rosyperiwi}
.....G.....
HMGRclustalW{ tomato}
.....G.....
HMGRclustalW{woodtobacc}
.....G.....
HMGRclustalW{ potato}
.....
HMGRclustalW{radish}
.....
HMGRclustalW{arabadopsis1}
.....
HMGRclustalW{cucumismel}
.....
HMGRclustalW{rubbertre2}
.....
HMGRclustalW{rubbertre1}
.....
HMGRclustalW{camptothec}
.....
HMGRclustalW{arabadops2}
.....
HMGRclustalW{chineseham}	KN..PITSPV VTPKKAPDNC CRREPLLVRK SEKLSSVEEE
PGVSQDRKVE	

FIG. 32V

HMGRclustalW{chineseha2}	KN..PITSPV	VTPKKAPDNC	CRREPLLVR	SEXLSSVEEE
PGVSQDRKVE				
HMGRclustalW{syrianhamst}	KN..PITSPV	ATPKKAPDNC	CRREPVLRR	NEKLSSVEEE
PGVNQDRKVE				
HMGRclustalW{rat}	KN..PITSPV	VTPKKAQDNC	CRREPLLVR	NQKLSSVEED
PGVNQDRKVE				
HMGRclustalW{rabbit}	KN..PITSPV	VTQKKVPDSC	CRREPVVVRN	NQKFCSSVEEE
AGMSQDRKVE				
HMGRclustalW{human}	KN..PITSPV	VTQKKVPDNC	CRREPMLVRN	NQKCDSSVEEE
TGINRERKVE				
HMGRclustalW{mouse}
.....				
HMGRclustalW{xenopus}	KN..PITSPV	AVQKKQIESC	CRREPEQ.EK	TVHVSSTEEA
S..SKEETEA				
HMGRclustalW{sea urchin}	MEGHEVVNPG	SDHEDASEVE	TIGTLSSSPS	TSDVRVIESM
TSRTQACQID				
HMGRclustalW{cockroach}	VTGDSVVNSN	STDDAQLHY	IMRWLTV..S	ADHIVILILL
LALAVKFVFF				
HMGRclustalW{drosophila}	RQ....SGPV	AIEAKASQTT	PIDEEHVE..QEKD
TENSAAVRTL				
HMGRclustalW{dictyostel}
.....				
HMGRclustalW{schistosom}	YEVTSIFHFI	YNIFHVINAN	LVVYLFGLGF	LFKRIRLNKP
INSQLRNINI				
HMGRclustalW{archaeoglo}
.....				
HMGRclustalW{pseudomonas}
.....				
Consensus	KN--PITSPV	VT-KKAPDNC	CRREPLLVR	--K-SSVEEE, -G-
SQDRKVE				

FIG. 32W

600	551
EMGRclustalW{methanobac}
EMGRclustalW{methanococ}
EMGRclustalW{halobacter}
EMGRclustalW{sulfolobus}
EMGRclustalW{ yeast2}	LVVQOKSATI EFSET..... RSMPTA SSGLETPVTA
KDIIISEEIQ	
EMGRclustalW{ yeast1}	TAPVQKASTP VLTN..... KTVIS GSKVKSLSSA
QSSSSGPPSS	
EMGRclustalW{phycomycetes}
EMGRclustalW{ fusarium}	LPLGEYVPPT PMRTQ..... PSTPA ITDDEAEG..
..LHMTKARP	
EMGRclustalW{ candida}	LKPKKKQASK TAVSV..... PKAVV VKDSETTKSS
EILHSSSESE	
EMGRclustalW{dictyoste2}	..KGKSVNVE DLKDQ..... EIIAL VDKGEIQP..
...HNLETRL	
EMGRclustalW{wheat1}
EMGRclustalW{ rice}GQG GSR..... ..RA.....A
PPEPAPMHGH	
EMGRclustalW{ corn}SSGS AAA..... ..PSRQHAQA
PAPCELLGSP	
EMGRclustalW{wheat3}
EMGRclustalW{wheat2}
EMGRclustalW{ soybean}
EMGRclustalW{rubbertre3}PTG AC..... ..AAPSLDCS
LSLPTXIHAP	
EMGRclustalW{rosyperiwi}	..T..NCTTL GC..... ..AVPPPSVP
KIAPVVPQQP	
EMGRclustalW{ tomato}	..P...ATTTL GC..... ..AVPAPPAR
QIAPMAAPPQ	
EMGRclustalW{woodtobacc}	..P...ATTTL GCT..... ..AVPPPPAL
QIVPMVPPQP	
EMGRclustalW{ potato}	..PCAAATTTL GC..... ..VVPPPPVR
KIAPMVPPQP	
EMGRclustalW{radish}LVTC PPP..... ..PPP.....S
QIVAAKLPPN	
EMGRclustalW{arabidopsis1}LVTC SPP..... ..TP.....
IVSVAKLPNP	
EMGRclustalW{cucumismel}LIDN NRY..... ..AAPRSASA
VALPSKVDA	
EMGRclustalW{rubbertre2}
EMGRclustalW{rubbertrel}LVTC PPA..... ..NISTKTTI
IAAPTKLPTS	
EMGRclustalW{camptothec}TVP CAA..... ..APVDCPLP
PIKPKVVDV	
EMGRclustalW{arabidopsis2}MIPC NQ..... ..SLDCREVL
PIKPNVDP	
EMGRclustalW{chineseham}	VIKPLVVETE SAS..... .RATFVLG.A .SGTSPPVAA
RTQELZELP	

FIG. 32X

HMGRclustalW{chineseha2}	VIKPLVVETE SAS.....	.RATFVLG.A	.SGTSPPVAA
RTQELEIELP			
HMGRclustalW{syrianhamst}	VIKPLVAETE STS.....	.RATFVLG.A	.SGGCSPVAL
GTQEPEIELP			
HMGRclustalW{ rat}	VIKPLVAEAE TSG.....	.RATFVLG.A	.SAASPPLAL
GAQEPGIELP			
HMGRclustalW{ rabbit}	VIKPLVAETD SPH.....	.RAAFVVGGS	.SFPDTSVL
ETKEPEIELP			
HMGRclustalW{ human}	VIKPLVAETD TPN.....	.RATFVVGNS	.SLLDTSVL
VTQEPEIELP			
HMGRclustalW{ mouse}		
.....			
HMGRclustalW{ xenopus}	VIKPLPLETS P.....	.KAKFIVG..	.DSSPLELSP
EDKNTMFDLP			
HMGRclustalW{sea urchin}	PVTASPRNSR SSSPVSSHVS	KPARFTIGSS	GSSEDEEEE
VIKEEVEWV			
HMGRclustalW{ cockroach}	ETRDELTTTR GMDG.....	W VEVSSPVEHK	YVQTEQPSCS
APEQPLEEPP			
HMGRclustalW{drosophila}	LFTIEDQSSA N.....		..ASTQTDLL
PLRHRLVGPI			
HMGRclustalW{dictyostel}SGKEQ EQ.....		..QQQQQQQQ
QQTPDITNQP			
HMGRclustalW{schistosom}	PKIKETLISD QVKQSPVLPK	FSKKLNDIPL	QSRKRIYCLH
KDDDYIDRND			
HMGRclustalW{archaeoglo}		
.....			
HMGRclustalW{pseudomonas}		
.....			
	Consensus	VIKPLVAETE --S-----	-RATFV-G-A -SA-PPPPA- -I-
PPEIELP			

FIG. 32Y

650	601
HMGRclustalW{methanobac}MS.
...IMDDLME	
HMGRclustalW{methanococ}MEN
YNDILEKMLN	
HMGRclustalW{halobacter}MTD
AASLADRVRE	
HMGRclustalW{sulfolobus}MK.
IDEVVEKLVK	
HMGRclustalW{ yeast2}	NNE.CVYALS SQDEPIRP.L SNLVELME.. ..KEQLKNNM
NTEVSNLVVN	
HMGRclustalW{ yeast1}	SEEDDSRDIE SLDKKIRP.L EELEALLS.. ..SGNTKQLK
NKEVAALVIH	
HMGRclustalW{phycomycetes}
.....	
HMGRclustalW{ fusarium}	ANL.....PNRS.N EELEKLLS.. ..ENALREMT
DEEVISLSMR	
HMGRclustalW{ candida}	SEQ.....SSRP.L EQVIELYK.. ..DGK/KTLV
DDEVVSLVTA	
HMGRclustalW{dictyoste2}	PNN.....F QRAVHIRR.. ..KLLARDLQ
KEHQRALHAQ	
HMGRclustalW{wheat1}
.....	
HMGRclustalW{ rice}	G.....GGMMEGD
DEEIVAAVAS	
HMGRclustalW{ corn}	AA.....A.. ..PEKMPED
DEEIVASVVA	
HMGRclustalW{wheat3}
.....	
HMGRclustalW{wheat2}
.....	
HMGRclustalW{ soybean}
.....	
HMGRclustalW{rubbertre3}I VSTTT.....TSTLSDD
DEQIIKSVVS	
HMGRclustalW{rosyperiwi}	SK.....MV.I IEKPAPLI.. ..TPQNSEE
DEDIIKAVVA	
HMGRclustalW{ tomato}	S.....MS.M VEKPAPLI.. ..TSASSGE
DEEIIKSVVQ	
HMGRclustalW{woodtobacc}	SKV.....AA.M SEKPAPLV.. ..TPAASEE
DEEIIKSVVQ	
HMGRclustalW{ potato}	AKV.....ALS.Q TEKPSPII.. ..MPALSED
DEEIIQSVVQ	
HMGRclustalW{radish}	E.....QPPLPKE
DEEIVKSVLD	
HMGRclustalW{arabadosis1}	EP.....IV.. ..TESLPEE
DEEIVKSVID	
HMGRclustalW{cucumismel}	EA.....LN.. ..TIPLPEE
DEEVVKMVVD	
HMGRclustalW{rubbertre2}
.....	
HMGRclustalW{rubbertre1}	EP.....LI.. ..APLVSEE
DEMIVNSVVD	
HMGRclustalW{camptothec}	P.....I.. ..SPPSSEE
DEEIIKSVVE	
HMGRclustalW{arabados2}	RE.....SELDSVE
DEEIVKLVID	
HMGRclustalW{chineseham}	SE.....PRP.N EECLQILE.. SAEKGAKFLS
DAEIIQLVNA	

FIG. 32Z

HMGRclustalW{chineseha2}	SE.....	PRP.N	EECLQILE..	SAEKGAKFLS
DAEIIQLVNA				
HMGRclustalW{syrianhamst}	SE.....	PRP.N	EECLQILE..	SAEKGAKFLS
DAEIIQLVNA				
HMGRclustalW{ rat}	SE.....	PRP.N	EECLQILE..	SAEKGAKFLS
DAEIIQLVNA				
HMGRclustalW{ rabbit}	KE.....	PRP.N	EECLQILG..	NAEKGAKFLS
DAEIIQLVNA				
HMGRclustalW{ human}	RE.....	PRP.N	EECLQILG..	NAEKGAKFLS
DAEIIQLVNA				
HMGRclustalW{ mouse}			
.....				
HMGRclustalW{ xenopus}	EE.....	PRP.L	DECVRILK..	NPDKGAQYLT
DAEIVISLVNA				
HMGRclustalW{sea urchin}	LET.....	ELKAPRP.M	PELLEIL...	NVGKGPNAIT
DDEVQLLVGA				
HMGRclustalW{ cockroach}	AS.....	NRS.I	DECLSVC...	KSDVGAQALS
DCEVMALVTS				
HMGRclustalW{drosophila}	KP.....	PRP.V	QECLDILNST	EEGSGPAALS
DEEIVSIVHA				
HMGRclustalW{dictyostel}	TKTN.....			.KKIPIKELS
NEEILIKLEK				
HMGRclustalW{schistosom}	SSSVSTFSNT	CKNSNERPSN	VLDLDMLTEK	IKQGLGHELS
DTEILQLLSH				
HMGRclustalW{archaeoglo}			
.MQVLRLLDRR				
HMGRclustalW{pseudomonas}			
.....				
DEEIIKLVA	Consensus	SE-----	-----PRP-N	EECLQIL--- -AEKGAKSLS

FIG. 32AA

700

HMGRclustalW{methanobac} GR..IKLYEI E.RHVPVDEA VRIRREFIE.RTCGVK
 ..LEHVSNY
 HMGRclustalW{methanococ} GE..IKPYQL D.KMFGSKIA TEIRRKPIE.KKVGIE
 ..FKHICNY
 HMGRclustalW{halobacter} GD..LRLHEL E.AHADADTA AEARRLLVE.SQSGAS
 ..LDAVGNYG
 HMGRclustalW{sulfolobus} GE..ISFHEV D.NLLEANAA MVARRLALE.KIVGVG
 ..LPSIGSTV
 HMGRclustalW{ yeast2} G..KLPLYSL EKKLEDTTRA VLVRRKALST LAESPILVS.
 ...EKLPFRN
 HMGRclustalW{ yeast1} G..KLPLYAL EKKLGDTTTRA VAVRRKALSI LAEAPVLAS.
 ...DRLPYKN
 HMGRclustalW{phycomyces}

 HMGRclustalW{ fusarium} G..KIPGYAL EKTLDGDFTRA VKIRRSIIAR NKAADITHS
 LDRSKLPYEN
 HMGRclustalW{ candida} G..KLPLYAL EKQLGDNLRA VAIRRKALSD LADAPVLRS.
 ...NKLPYLH
 HMGRclustalW{dictyoste2} A..VVAAAEK AATSGEDPSS IQPVVPPTSN LDFEGSLTN.
LPVDH
 HMGRclustalW{wheat1}

 HMGRclustalW{ rice} G..ALPSHRL ESRLGDCRRA ARLPREALR.RVTGRG
 ..VEGLPFDG
 HMGRclustalW{ corn} G..KVPSYAL EARLGDCRRA AGIRREALR.RITGRD
 ..IEGLPLDG
 HMGRclustalW{wheat3}

 HMGRclustalW{wheat2}

 HMGRclustalW{ soybean}

 HMGRclustalW{rubbertre3} G..SIPSYSL ESKLGNCKRA ALIRRETLQ.RMSGRS
 ..LEGLPLDG
 HMGRclustalW{rosyperiwi} G..KIPSYSL ESKLGDCCKRA AGIRREALQ.RITGKS
 ..LEGLPLEG
 HMGRclustalW{ tomato} G..KIPSYSL ESKLGDCCKRA ASIRKEVMQ.RITGKS
 ..LEGLPLEG
 HMGRclustalW{woodtobacc} G..KMPSYSL ESKLGDCCKRA ASIRKEALQ.RITGKS
 ..LEGLPLEG
 HMGRclustalW{ potato} G..KTPSYSL ESKLGDCMRA ASIRKEALQ.RITGKS
 ..LEGLPLEG
 HMGRclustalW{radish} G..VVPYSL ESRLGDCCKRA ASIRREALQ.RLTGRS
 ..IEGLPLDG
 HMGRclustalW{arabadopsis1} G..VIPSYSL ESRLGDCCKRA ASIRREALQ.RVTGRS
 ..IEGLPLDG
 HMGRclustalW{cucumismel} G..SVPSYSL ESKLGDPKRA ASIRREALQ.RTTGRS
 ..IHGLPFEG
 HMGRclustalW{rubbertre2}

 HMGRclustalW{rubbertre1} G..KIPSYSL ESKLGDCCKRA AAIRREALQ.RMTRRS
 ..LEGLPVEG
 HMGRclustalW{camptothec} G..TTPSYAL ESKLGDSHRA AAIRREALQ.RMTKKS
 ..LAGLPLDG
 HMGRclustalW{arabadops2} G..TIPSYSL ETKLGDCCKRA AAIRREAVQ.RITGKS
 ..LTGLPLEG
 HMGRclustalW{chineseham} K..HIPAYKL ETLMETHERG VSIRRQLLST K..LPEPSS.
 ..LQYLPYRD

FIG. 32BB

```

HMGRclustalW(chineseha2} K..HIPAYKL ETLMETHERG VSIRRQLLST K..LPEPSS.
..LQYLPYRD
HMGRclustalW(syrianhamst} K..HIPAYKL ETLMETHERG VSIRRQLLST K..LPEPSS.
..LQYLPYRD
HMGRclustalW( rat} K..HIPAYKL ETLMETHERG VSIRRQLLSA K..LAEPSS.
..LQYLPYRD
HMGRclustalW( rabbit} K..HIPAYKL ETLMETHERG VSIRRQLLSK K..LPEPSS.
..LQYLPYRD
HMGRclustalW( human} K..HIPAYKL ETLMETHERG VSIRRQLLSK K..LSEPSS.
..LQYLPYRD
HMGRclustalW( mouse} .....
.....
HMGRclustalW( xenopus} K..HIPAYKL ETMMESPREG VAIRRQMLSD K..LPQRSA.
..LQSLPYKN
HMGRclustalW(sea urchin} K..HIPAYKL ENILDNPERG VAVRRQIISK L..LPITDA.
..LEKLPYAS
HMGRclustalW( cockroach} G..HIAGYQL EKVRNPERG VGIRRQILTK T..ADLKDA.
..LDNLPYKN
HMGRclustalW(drosophila} GGTHCPLHKI ESVLDDPERG VRIRRQIIGS R..AKMPVGR
..LDVLPYEH
HMGRclustalW(dictyostel} G..EVLAYRL ENELGDCSRA VEIRRMLEX ....QLSKK.
..IEPIPEG
HMGRclustalW(schistosom} G..RLKTREL ESVVRNPFRA VELRRLDLS. ....TFLNNP
HIIRIPYKD
HMGRclustalW(archaeoglo} HYKSGKIRRA MSSRIPGFYK LSVEERLKKV AEFAGLSDEE
..VKAVLSQG
HMGRclustalW(pseudomonas} .....MS LDSRLPAFRN LSPAARLDHI GQLLGLSHDD
..VSLLANAG

Consensus G---IPSYSL ESKLGDCKRA VSIRREALSK K--LRITGSS --
LEGLPYEG

```


FIG. 32CC

750		701
HMGRclustalW{methanobac}		IDMERASRRN IENPIGVVQI PLGVAGPLRV RGEHADGEYY
VPLATSEGA		
HMGRclustalW{methanococ}		IDEEMAMKGN IENMIGAIQI PLGFAGPLKI NGEYAKGEFY
IPLATTEGA		
HMGRclustalW{halobacter}		FPAEAAES.A IENMVGSIQV PMGVAGPVSV DGGSVAGEKY
LPLATTEGA		
HMGRclustalW{sulfolobus}		IDYSEIKNKN AENVIGAIQI PLGIVGPIRV NGDYAKGDFY
VPMATTEGA		
HMGRclustalW{	yeast2}	YDYDRVFGAC CENVIGYMPI PVGVIGPLII DGT....SYH
IPMATTEGCL		
HMGRclustalW{	yeast1}	YDYDRVFGAC CENVIGYMPL PVGVIGPLVI DGT....SYH

FIG. 32DD

```

IPMATTEGCL
  HMGRclustalW{phycomyces} .....
.PMATTEGCL
  HMGRclustalW{ fusarium} YNWERFFGAC CENVIGYMPL PVGVAGPLVI DGQ....SYF
IPMATTEGCL
  HMGRclustalW{ candida} YDYDRVFGAC CENVIGYMPL PVGVAGPLII DGK....PYH
IPMATTEGCL
  HMGRclustalW{dictyoste2} FDYTKVLGAC CENVIGYIPI PVGVAGPILL DGK....LVS
IPMATTEGCL
  HMGRclustalW{wheat1} .....
.....
  HMGRclustalW{ rice} MDYQAILGQC CEMPVGIVVQL PVGVAGPLLL DGR....EYH
VPMATTEGCL
  HMGRclustalW{ corn} FDYASILGQC CELPVGVVQL PVGVAGPLLL DGR....RFY
LPMATTEGCL
  HMGRclustalW{wheat3} .....
.....
  HMGRclustalW{wheat2} .....
.....
  HMGRclustalW{ soybean} .....
.....
  HMGRclustalW{rubbertre3} FDYESILGQC CEMAIGYVQI PVGIAGPLLL DGK....EYT
VPMATTEGCL
  HMGRclustalW{rosyperiwi} FDYASILGQC CEMPVGIVVQL PVGIAGPLLL DGR....EYM
LPMATTEGCL
  HMGRclustalW{ tomato} FNYESILGQC CEMPIGYVQI PVGIAGPLLL NGK....EFS
VPMATTEGCL
  HMGRclustalW{woodtobacc} FDYESILGQC CEMPIGYVQI PVGIAGPLLL DGR....EYS
VPMATTEGCL
  HMGRclustalW{ potato} FDYSSILGQC CEMPVGIVVQI PVGIAGPLLL DGR....EYS
VPMATTEGCL
  HMGRclustalW{radish} FDYDSILGQC CEMPVGIVQI PVGIAGPLLL DGY....EYS
VPMATTEGCL
  HMGRclustalW{arabadosis1} FDYESILGQC CEMPVGIVQI PVGIAGPLLL DGY....EYS
VPMATTEGCL
  HMGRclustalW{cucumismel} FDYESILGQC CEMPVGIVVQI PVGIAGPLLL DGF....EYT
VPMATTEGCL
  HMGRclustalW{rubbertre2} .....
.....
  HMGRclustalW{rubbertre1} FDYESILGQC CEMPVGIVVQI PVGIAGPLLL NGR....EYS
VPMATTEGCL
  HMGRclustalW{camptothec} FDYDSILGQC CEMPVGIVVQI PVGIAGPLLL DGR....EYS
VPMATTEGCL
  HMGRclustalW{arabados2} FDYNSILGQC CEMPVGIVVQI PVGIAGPLLL DGV....EYS
VPMATTEGCL
  HMGRclustalW{chineseham} YNYSLVMGAC CENVIGYMPI PVGVAGPLCL DGK....EYQ
VPMATTEGCL
  HMGRclustalW{chineseha2} YNYSLVMGAC CENVIGYMPI PVGVAGPLCL DGK....EYQ
VPMATTEGCL
  HMGRclustalW{syrianhamst} YNYSLVMGAC CENVIGYMPI PVGVAGPLCL DGK....EYQ
VPMATTEGCL
  HMGRclustalW{ rat} YNYSLVMGAC CENVIGYMPI PVGVAGPLCL DGK....EYQ
VPMATTEGCL
  HMGRclustalW{ rabbit} YNYSLVLGAC CENVIGYMPI PVGVVGPLCL DGK....EFQ
VPMATTEGCL
  HMGRclustalW{ human} YNYSLVMGAC CENVIGYMPI PVGVAGPLCL DEK....EFQ
VPMATTEGCL
  HMGRclustalW{ mouse} .....
.....
  HMGRclustalW{ xenopus} YNYSLVMGAC CENVIGYMPI PVGVAGPLLL NNK....EYQ

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FIG. 32EE

VPMATTEGCL			
HMGRclustalW{sea urchin}	YDYSFVSGAC	CENVIGYMPV	PVG VAGPLLL DGQ....EFQ
VPMATTEGCL			
HMGRclustalW{ cockroach}	YDYLKVMGAC	CENVIGYMPV	PVG VAGPLNL DGR....LVH
VPLATTEGCL			
HMGRclustalW{drosophila}	FDYRKVLNAC	CENVLGYVPI	PVG YAGPLLL DGE....TTY
VPMATTEGAL			
HMGRclustalW{dictyostel}	FDFAKVQGQC	CENVIGYVPI	PVG TAGPIQL NGQ....LVT
IPMATTEGCL			
HMGRclustalW{schistosom}	YDYRLVYGQC	CEEVIGYMPI	PVG KIGPLLL DGR....SHY
IPLATTEGCL			
HMGRclustalW{archaeoglo}	.LPLDVADRM	IENVIGTFEL	PLGIATNFLI DGK....DYL
IPMAIEEPSV			
HMGRclustalW{pseudomonas}	ALPMDIANGM	IENVIGTFEL	PYAVASNFQI NGR....DVL
VPLVVEPSI			
	Consensus	FDY-SVLG-C	CENVIGY--I PVG VAGPLLL DGK----EYS
<u>VPMATTEGCL</u>			

HMGCoA binding

E

FIG. 32FF

800	751
HMGRclustalW{methanobac}	VASVNRGCSV ITRAGGATVR VTGDSMT.RA PVIRTGSVVE
ALQLREWIYE	
HMGRclustalW{methanococ}	VASVNRGCSI ITKCGGATVR VIDDKMT.RA PCLKTKSVVD
AIKVRDWIRE	
HMGRclustalW{halobacter}	LASVNRGCSV INSAGGATAR VLKSGMT.RA PVFRVADVAE
AEALVSWTRD	
HMGRclustalW{sulfolobus}	IASVNRGIKA VTLSGGVRAK VLKDEMT.RA PVFKFDSIEQ
IPNFLKFIEE	
HMGRclustalW{ yeast2}	VASAMRGCKA INAGGGATTV LTKDGMT.RG PVVRFPTLIR
SGACKIWLDS	
HMGRclustalW{ yeast1}	VASAMRGCKA INAGGGATTV LTKDGMT.RG PVVRFPTLKR
SGACKIWLDS	
HMGRclustalW{phycomycetes}	VASTARGCKA INAGGGASTI VIADGMT.RG PCVEFPTILR
AAACKLWIEN	
HMGRclustalW{ fusarium}	VASASRGCKA INSGGGAITV LTADGMT.RG PCVAFETLER
AGAAKLWLDS	
HMGRclustalW{ candida}	VASAMRGCKA INLGGGVTTV LTKDGMT.RG PCVKFPSLKR
AGQCKLWLDS	
HMGRclustalW{dictyoste2}	VASTHRGAKA ITKSGGAKTV LLQSGMT.RA PVCRLPSSIR
AGELKQWIEN	
HMGRclustalW{wheat1}
.....	
HMGRclustalW{ rice}	VASVNRVQV HLVSGGAFSV LLRDAMS.RA PAVKLPCPME
AAELKAFAEA	
HMGRclustalW{ corn}	VASTNRGCKA IAESGGATSV VLRDAMT.RA PVARFPTARR
AAELKAFLED	
HMGRclustalW{wheat3}
.....	
HMGRclustalW{wheat2}
.....	
HMGRclustalW{ soybean}
.....	
HMGRclustalW{rubbertre3}	VASANRGCKA IYASGGATSV LLRDGMT.RA PVVRFPTAKR
AADLKFFMED	
HMGRclustalW{rosyperiwi}	VASTNRGCKA ILASGGANSV LLRDGMT.RA PVVRFGTAKR
AAELKFYMED	
HMGRclustalW{ tomato}	VASTNRGCKA IYASGGATCI LLRDGMT.RA PCVRFGTAKR
AAELKFFVED	
HMGRclustalW{woodtobacc}	VASTNRGCKA IYASGGATSV LLRDGMT.RA PCVRFGTAKR
AAELKFFVED	
HMGRclustalW{ potato}	VASTNRGCKA IFVSGGADSV LLRDGMT.RA PVVRFPTAKR
AAELKFFVED	
HMGRclustalW{radish}	VASTNRGCKA MYVSGGATST VLKDGMT.RA PVVRFASARR
ASELKFFLES	
HMGRclustalW{arabadopsis1}	VASTNRGCKA MFISGGATST VLKDGMT.RA PVVRFASARR
ASELKFFLEN	
HMGRclustalW{cucumismel}	VASTNRGCKA IYASGGATSM LLKDGMT.RA PVVRFSGAKR
ASELKFFLED	
HMGRclustalW{rubbertre2}
.....	
HMGRclustalW{rubbertre1}	VASTNRGCKA IYLSGGATSV LLKDGMT.RA PVVRFASATR
AAELKFFLED	
HMGRclustalW{camptothec}	VASTNRGCKA IFACGGATSV LLRDAMT.RA PVVRFSGAKR
AADLKFFLEN	
HMGRclustalW{arabadopsis2}	VASTNRGCKA IHLGGGAFSV LVKDAMT.RA PVVRFPSARR
AALVMFYLQD	
HMGRclustalW{chineseham}	VASTNRGCRA IGLGGGASSR VLADGMT.RG PVVRLPRACD
SAEVKAWLET	

FIG. 32GG

HMGRclustalW{chinese2}	VASTNRGCRA IGLGGGASSR VLADGMT.RG PVVRLPRACD
SAEVKAWLET	
HMGRclustalW{syrianhamst}	VASTNRGCRA IGLGGGASSR VLADGMT.RG PVVRLPRACD
SAEVKAWLET	
HMGRclustalW{ rat}	VASTNRGCRA ISLGGGASSR VLADGMS.RG PVVRLPRACD
SAEVKSWLET	
HMGRclustalW{ rabbit}	VASTNRGCRA ICLGGGASSR VLADGMT.RG PVVRLPRACD
SAEVKAWLET	
HMGRclustalW{ human}	VASTNRGCRA IGLGGGASSR VLADGMT.RG PVVRLPRACD
SAEVKAWLET	
HMGRclustalW{ mouse}
.....	
HMGRclustalW{ xenopus}	VASTNRGCRA IMLGGGAKSR VLADGMT.RG PVVRLPTACD
AAEVKAWLDS	
HMGRclustalW{sea urchin}	VASTNRGCRA LRSAGGIHSV LIGDGMT.RG PLVRLPSAQE
AGAIKQWLEV	
HMGRclustalW{ cockroach}	VASTNRGMRA LMRG.VTSR IVADGMT.RG PVVRFPNIDR
ASEAMLWMQV	
HMGRclustalW{drosophila}	VASTNRGCKA LSVRG.VRSV VEDVGMT.RA PCVRFPSVAR
AAEAKSWIEN	
HMGRclustalW{dictyostel}	VASTNRGCKA ITESGGAXCT ITSGMT.RA PVVRFSDIVK
ASEFVSWIND	
HMGRclustalW{schistosom}	VASTNRGCRA IFLAGGIKSV VYRDQMT.RA PVVWFPSIID
SVKCIWIDS	
HMGRclustalW{archaeoglo}	VAAASNAARM ARESGGFTTD YTGSLMIGQI QVTKLLNPNA
AKFEVLRQKD	
HMGRclustalW{pseudomonas}	VAAASYMAKL ARANGGFTTS SSAPLMHAQV QIVGIQDPLN
ARLSLLRRKD	
Consensus	VASTNRGCKA I-LSGGATSV VLADGMT-RA PVVRFPSAKR
AAELKFWLED	

FIG. 32HH

850	801
HMGRclustalW{methanobac}	NM..DALREE AESTTRHGKL VKIDPI.... IVAGSYVYPR
FVYTTGDSMG	
HMGRclustalW{methanococ}	NF..ERIKEV AESTTRHGKL IKIEPI.... LIVGRNLYPR
FVFKTGDAMG	
HMGRclustalW{halobacter}	NF..AALKEA AEETTTHGEL LDVTP..... YVVGNSVYLR
FRYDTKDAMG	
HMGRclustalW{sulfolobus}	NL..EKIRNI ANSTSHHGKL KSITP..... FVLGNNVWLR
FSFETGDAMG	
HMGRclustalW{ yeast2}	EEGQNSIKKA FNSTSRFARL QHIQT..... CLAGDLLFMR
FRTTTGDAMG	
HMGRclustalW{ yeast1}	EEGQNAIKKA FNSTSRFARL QHIQT..... CLAGDLLFMR
FRTTTGDAMG	
HMGRclustalW{phycomyces}	EG.NDIVTNA FNSTSRFARL RKLKI..... ALAGKLVFIR
FSTTTGDAMG	
HMGRclustalW{ fusarium}	EAGQDMMKKA FNSTSRFARL QSMKT..... ALAGTNLYIR
FKTTTGDAMG	
HMGRclustalW{ candida}	DEGQEEMKKA FNSTSRFARL QHLQT..... ALAGDLLFIR
FRTVTGDAMG	
HMGRclustalW{dictyoste2}	QENFYQVASA FNSTSRFARL KSIKV..... VIAGRLVYLR
FKSSTGDAMG	
HMGRclustalW{wheat1}
.....GDAMG	
HMGRclustalW{ rice}	PANFELLA AV FNRSSRFARL QDIRC..... ALAGRNLYMR
FSCITGDAMG	
HMGRclustalW{ corn}	PANFDTLSVV FNRSSRFARL QGVQC..... AMAGRNLYMR
FSCSTGDAMG	
HMGRclustalW{wheat3}
.....GDAMG	
HMGRclustalW{wheat2}
.....GDAMG	
HMGRclustalW{ soybean}
.....	
HMGRclustalW{rubbertre3}	PDNFDTIAVV FNKSSRFARL QSVQC..... AIAGKNLYMR
FSCSTGDAMG	
HMGRclustalW{rosyperiwi}	TQNFETISVV FNKSSRFAXL QSVQC..... AIAGKNLYIR
FSCSTGDAMG	
HMGRclustalW{ tomato}	PIKFESLANV FNQSSRFARL QRIQC..... AIAGKNLYMR
LCCSTGDAMG	
HMGRclustalW{woodtobacc}	PVKFETLAAV FNQSSRFARL QRIQC..... AIAGKNLYMR
FVCSTGDAMG	
HMGRclustalW{ potato}	PLNFETLSLM FNKSSRFARL QGIQC..... AIAGKNLYIT
FSCSTGDAMG	
HMGRclustalW{radish}	PENFETLAVV FNRSSRFARL QSVMC..... TLAGKNAYVR
FSCSTGDAMG	
HMGRclustalW{arabidopsis1}	PENFDTLAVV FNRSSRFARL QSVKC..... TIAGKNAYVR
FCCSTGDAMG	
HMGRclustalW{cucumismel}	PSNFDTLAVV FNRSSRFARL QSIRC..... SIAGKNLYVR
FCCSTGDAMG	
HMGRclustalW{rubbertre2}
.....	
HMGRclustalW{rubbertrel}	PDNFDTLAVV FNKSSRFARL QGIKC..... SIAGKNLYIR
FSCSTGDAMG	
HMGRclustalW{camptothec}	PLNFETLAAV FNSSSRFGKL QNIKC..... AIAGKNLYMR
YSCSTGDAMG	
HMGRclustalW{arabidops2}	PSNFERLSLI FNKSSRFARL QSITC..... TIAGRNLYPR
FACSTGDAMG	
HMGRclustalW{chineseham}	PEGFAVIKDA FDSTSRFARL QKLHV..... TMAGRNLYIR
FQSKTGDAMG	

FIG. 32II

HMGRclustalW{chineseha2}	PEGFAVIKDA	FDSTSRFARL	QKLHV.....	TMAGRNLVIR
FQSKTGDAMG				
HMGRclustalW{syrianhamst}	PEGFAVIKDA	FDSTSRFARL	QKLHV.....	TMAGRNLVIR
FQSKTGDAMG				
HMGRclustalW{ rat}	PEGFAVVKEA	FDSTSRFARL	QKLHV.....	TLAGRNLVIR
LQSKTGDAMG				
HMGRclustalW{ rabbit}	PEGFAVIKEA	FDSTSRFARL	QKLHI.....	SMAGRNLVIR
FQSKTGDAMG				
HMGRclustalW{ human}	SEGFAVIKEA	FDSTSRFARL	QKLHT.....	SIAGRNLVIR
FQSRSGDAMG				
HMGRclustalW{ mouse}
.....				
HMGRclustalW{ xenopus}	AEGFKVIKDA	FDSTSRFARL	GRLQN.....	CVAGRNLVIR
FQSKTGDAMG				
HMGRclustalW{sea urchin}	PENFAAIKER	FESTSRFAKL	KSIQT.....	ALAGRYMFLR
FKALTGDAMG				
HMGRclustalW{ cockroach}	PYNFEQIKKN	FDSTSRFARL	SKIHI.....	RVAGRHLFIR
FIATTGDAMG				
HMGRclustalW{drosophila}	DENYRVVXTE	FDSTSRFGRL	KDCHI.....	AMDGPQLVIR
FVAITGDRMG				
HMGRclustalW{dictyostel}	TDNYQALKAV	FDSTSRFARL	SAIKC.....	TIAGRSVYIR
FKCDTGDAMG				
HMGRclustalW{schistosom}	EEGFQTLKSA	FDKTSAHVNL	LSVFA.....	CPAGRYIHIR
FAARTGDAMG				
HMGRclustalW{archaeoglo}	EIIERANECD	PMLVNLGGGC	KDIEAR.VID	TIMGKMLIVH
LIVDVKDAMG				
HMGRclustalW{pseudomonas}	EIIELANRKO	QLLNSLGGGC	RDIEVETPAD	TPRGPMVAH
LIVDVRDAMG				
	Consensus	PENFETLK-A	FNSTSRFARL	QSIQC-----
FSCSTGDAMG				AIAGRNLVIR

NADE binding domain 1

(continued)

FIG. 32JJ

900
 HMGRclustalW{methanobac} MNMVTIATER ALELLT...R ETGAHV..IA LSGNLCSTDKK
 PAAVNWIEGR
 HMGRclustalW{methanococ} MNMVTIATEK ACNFIEGELK KEGIFVKIVA VSGNACVDDKK
 PSGMNLINGR
 HMGRclustalW{halobacter} MNMATIATEA VCGVVE...A ETAASL..VA LSGNLCSTDKK
 PAAINWIEGR
 HMGRclustalW{sulfolobus} MNMVTIAVEK VCEFIE.... ENFPSADCLA VSGNMCSTDKK
 QTNVNSLFGR
 HMGRclustalW{ yeast2} MNMISKGVEY SLKQMVVEY.. .GWEDMEVVS VSGNYCTDKK
 PAAINWIEGR
 HMGRclustalW{ yeast1} MNMISKGVEY SLKQMVVEY.. .GWEDMEVVS VSGNYCTDKK
 PAAINWIEGR
 HMGRclustalW{phycomycetes} MNM.....

 HMGRclustalW{ fusarium} MNMISKGVEH ALSVMANDG.. .GFDDMQIIS VSGNYCTDKK
 AAALNWIDGR
 HMGRclustalW{ candida} MNMISKGVEY ALKQMTVEF.. .GWDDMMVVS VSGNYCTDKK
 PAAVNWIEGR
 HMGRclustalW{dictyoste2} MNMVSKGVEK ALEVITEY.. .FPMEVLS LSGNYCTDKK
 PSSINWIEGR
 HMGRclustalW{wheat1} MNMVSKGVEN VLGYIRNN.. .FPDMDVIS ISGNYCSDKK
 ATAVNWIDGR
 HMGRclustalW{ rice} MNMVSKGVEN VLGYLQNV.. .FPDMDVIS VSGNYCSDKK
 PTAVNWIEGR
 HMGRclustalW{ corn} MNMVSKGVQN VLDLQDD.. .FHDMDVIS ISGNFCSDKK
 PSAVNWIEGR
 HMGRclustalW{wheat3} MNMISKGVN VLDYLQDD.. .FPDMDVIS ISGNFCSDKK
 PAAVNWIEGR
 HMGRclustalW{wheat2} MNMISKGVQH VLDYLEED.. .FPDMDVVS ISGNFCSDKK
 SAAVNWIEGR
 HMGRclustalW{ soybean}

 HMGRclustalW{rubbertre3} MNMVSKAVQN VIDYLQND.. .FPDMDVIG LTGNFCADKK
 AAAVNWIEGR
 HMGRclustalW{rosyperiwi} MNMVSKGVQN VLEFLQTD.. .YPDMDVLG ISGNFCADKK
 PAAVNWIEGR
 HMGRclustalW{ tomato} MNMVSKGVQN VLDYLQNE.. .YPDMDVIG ISGNFCSDKK
 PAAVNWIEGR
 HMGRclustalW{wood-tobacc} MNMVSKGVQN VLDYLQNE.. .YPDMDVIG ISGNFCSDKK
 PAAVNWIEGR
 HMGRclustalW{ potato} MNMVSKGVQN VLDYLQSE.. .YPDMDVIG ISGNFCSDKK
 PAAVNWIEGR
 HMGRclustalW{radish} MNMVSKGVQN VLEFLTED.. .FPDMDVIG ISGNFCSDKK
 PAAVNWIEGR
 HMGRclustalW{arabidopsis1} MNMVSKGVQN VLEYLTDD.. .FPDMDVIG ISGNFCSDKK
 PAAVNWIEGR
 HMGRclustalW{cucumismel} MNMVSKGVQN VLEFLQHD.. .FSDMEVIG ISGNFCADKK
 PAAVNWIEGR
 HMGRclustalW{rubbertre2}LESD.. .FADMDVIG ISGNFCSDKK
 PAAVNWIEGR
 HMGRclustalW{rubbertrel} MNMVSKGVQN VLEFLQSD.. .FSDMDVIG ISGNFCSDKK
 PAAVNWIEGR
 HMGRclustalW{camptothec} MNMISKGVN VLDLQDD.. .FPDMDVIG ISGNYCSDKK
 PAAVNWIEGR
 HMGRclustalW{arabidops2} MNMVSKGVQN VLDLVKSE.. .FPDMDVIG ISGNYCSDKK
 ASAVNWIEGR
 HMGRclustalW{chineseham} MNMISKGTEK ALLKLQEF.. .FPQMILA VSGNYCTDKK
 PAAINWIEGR

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FIG. 32KK

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HMGRclustalW{chineseha2} MNMISKGTEK ALLKLQEF... ..FPQMILA VSGNYCTDKK
PAAINWIEGR
HMGRclustalW{syrianhamst} MNMISKGTEK ALVKLQEF... ..FPQMILA VSGNYCTDKK
PAAVNWIEGR
HMGRclustalW{      rat} MNMISKGTEK ALLKLQEG... ..VPQLILA VSGNYCTDKK
PAAINWIEGR
HMGRclustalW{      rabbit} MNMISKGTEK ALSKLHEY... ..FPQMILA VSGNYCTDKK
PAAVNWIEGR
HMGRclustalW{      human} MNMISKGTEK ALSKLHEY... ..FPQMILA VSGNYCTDKK
PAAINWIEGR
HMGRclustalW{      mouse} .....EK ALLKLQEF... ..FPDMQILA VSGNYCTDKK
PAAINWIEGR
HMGRclustalW{      xenopus} MNMISKVTEQ ALARLQEE... ..FPDLFLVA VSGNYCTDKK
PAAINWIEGR
HMGRclustalW{sea urchin} MNMISKGTEQ ALHALQTM... ..FPNIEIMS LSGNYCTDKK
VAAINWIEGR
HMGRclustalW{cockroach} MNMLSKGTEV ALAYVQV... ..YPDMEILS LSGNFCTDKK
PAAVNWIEGR
HMGRclustalW{drosophila} MNMVSKALRW PFAEFTLH... ..FPDMQIIS LSGNFCCDKK
PAAINWIKGR
HMGRclustalW{dictyostel} MNMVSKGVEA VLEHLKII... ..FDDMTLLS ISGNMCTDKK
PSSINWIEGR
HMGRclustalW{schistosom} MNMVSKATDS ALHCLKKY... ..FSNMQVIS LSGNMCTDKK
PATINTILGR
HMGRclustalW{archaeoglo} ANAVNTMCEK VAPFIERITG .GKVYLRIS NLAAVRLARA
KAVFDKDVIG
HMGRclustalW{pseudomonas} ANTVNTMAEA VAPLMEAITG .GQVRLRILS NLADLRLARA
QVRITPQOLE

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Consensus MNMVSKGVEN VL--LQED-- -GFPDMQVIS ISGNYCTDKK
PAAVNWIEGR

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NADH binding domain 1 (concluded)

FIG. 32LL

950	901
HMGRclustalW{methanobac}	GKSITAEITV PGEMVESVLK TTPEAVVEVN TAKVLIGSAA
AG..SMG.FN	
HMGRclustalW{methanococ}	GKSIVAEVFL TEKEVNKYLK TTSQAIAEVN RLKQVIGSAI
SN..SMG.FN	
HMGRclustalW{halobacter}	GRSVTADVRI PREVVEERLE TTPERGRELN TRKNLVGSAA
AA..SLG.FN	
HMGRclustalW{sulfolobus}	GKTVLAEALI KKDVIRNHLH SNAQLIHDIN LRKNWLGTAR
AG..SLSQFN	
HMGRclustalW{ yeast2}	GKSVVAEATI PGDVVKSVLK SDVSALVELN ISKNLVGSAM
AG..SVGGFN	
HMGRclustalW{ yeast1}	GKSVVAEATI PGDVVRKVLK SDVSALVELN IAKNLVGSAM
AG..SVGGFN	
HMGRclustalW{phycomycetes}
.....	
HMGRclustalW{ fusarium}	GKGVVAEAII PGEVVRSVLK SDVDSLVELN VAKNLIGSAM
AG..SVGGFN	
HMGRclustalW{ candida}	GKSVVAEASI PKDAVVKVLK SSVKAVVDVN VNKNLIGSAM
AG..SVGGFN	
HMGRclustalW{dictyoste2}	GKSVVAEAVI SGDIVRDVLK TTVEALVSLN IDKNLIGSAM
AG..SIGGFN	
HMGRclustalW{wheat1}	GKSVVCEATI KGRVVQSVID TTVEKLVELN IIKNLAGSAV
AG..ALGGFN	
HMGRclustalW{ rice}	GKSVVCEAII KGDVVQKVLK TTVEKLVELN IIKNLAGSAV
AG..ALGGFN	
HMGRclustalW{ corn}	GKSVVCEAVI GEEVVKKVLK TDVQSLVELN TIKNLAGSAV
AG..ALGGFN	
HMGRclustalW{wheat3}	GKSVVCEAVI REELLKKVLK TNVQSLVELN VIKNLAGSAV
AG..ALGGFN	
HMGRclustalW{wheat2}	GKSVVCEAII REEVVEKVLK TNVQSLVELN VIKNLAGSAV
AG..ALGGFN	
HMGRclustalW{ soybean}LK TNVSALVELN MLKNLAGSAV
AG..ALGGFN	
HMGRclustalW{rubbertre3}	GKSVVCEAII KEEVVKKVLK TNVAALVELN MIKNLTGSAV
AG..SLGGFN	
HMGRclustalW{rosyperiwi}	GKSVVCEAII KEEIVKTVLK TEVAALIELN MVKNLAGSAI
AG..ALGGFN	
HMGRclustalW{ tomato}	GKSVVCEAII TEEVVKKVLK TEVAALVELN MLKNLTGSAM
AG..ALGGFN	
HMGRclustalW{woodtobacc}	GKSVVCEAII TEEVVKKVLK TEVAALVELN MLKNLTGSAM
AG..ALGGFN	
HMGRclustalW{ potato}	GKSVVCEAII KEEVVKKVLK TEVAALVELN MLKNLTGSAM
AG..ALGGFN	
HMGRclustalW{radish}	GKSVVCEAVI RGETVNKVLK TSVASLVELN MLKNLTGSAI
AG..SLGGFN	
HMGRclustalW{arabadosis1}	GKSVVCEAVI RGEIVNKVLK TSVAALVELN MLKNLAGSAV
AG..SLGGFN	
HMGRclustalW{cucumismel}	GKSVVCEAVI KDEVVRKVLK TSVASLVELN MLKNLTGSAM
AG..ALGGFN	
HMGRclustalW{rubbertre2}	GKSVVCEAII KEEVVKKVLK TDVALLVELN MLKNLAGSAV
AG..ALGGFN	
HMGRclustalW{rubbertre1}	GKSVVCEAII KEEVVKKVLK TNVASLVELN MLKNLAGSAV
AG..ALGGFN	
HMGRclustalW{camptothec}	GKSVVCEAVI KEEVVKKVLK TNVASLVELN MLKNLTGSAM
AG..ALGGFN	
HMGRclustalW{arabados2}	GKHVVCEAFI KAEIVKVLK TSVEALVELN TLKNLVGSAM
AG..SLGGFN	
HMGRclustalW{chineseham}	GKTVVCEAVI PAKVVRVLK TTTEAMIDVN INKNLVGSAM

FIG. 32MM

```

AG..SIGGYN
  HMGRclustalW{chineseha2} GKTIVCEAVI PAKVVREVLK TTTEAMIDVN INKQLVGSAM
AG..SIGGYN
  HMGRclustalW{syrianhamst} GKTIVCEAVI PARVVREVLK TTTEAMIDVN INKQLVGSAM
AG..SIGGYN
  HMGRclustalW{      rat} GKTIVCEAVI PAKVVREVLK TTTEAMVDVN INKQLVGSAM
AG..SIGGYN
  HMGRclustalW{      rabbit} GKTIVCEAVI PAKVVREVLK TTTEAMIDVN INKQLVGSAM
AG..SIGGYN
  HMGRclustalW{      human} GKSIVCEAVI PAKVVREVLK TTTEAMIEVN INKQLVGSAM
AG..SIGGYN
  HMGRclustalW{      mouse} GKTIVCEAVI PAKVVREVLK TTTEAMVDVN INKQLVGSAM
AG..SIGGYN
  HMGRclustalW{      xenopus} GKSIVCEAVI PAKVVREVLK SSTALVEVN INKQVFIGSAM
AG..SIGGYN
  HMGRclustalW{sea urchin} GKSIVCEATV PAHIVQQVLK TSASALVDLN IHAQLVGSAM
AG..SIGGFN
  HMGRclustalW{cockroach} GKSIVCEAIV PADIIKSVLK TSVQALMDVN ITAKLIGSAV
AG..SIGGFN
  HMGRclustalW{drosophila} GKRIVTECTI SAATLRVLK TDAKTLVECN KLAQMGGSAM
AG..SIGGFN
  HMGRclustalW{dictyostel} GRSIVCEAMI TGDVVQRLK TNVQALVDLN IAKVLIGSAM
AG..SIGGFN
  HMGRclustalW{schistosom} GKSIVAEHL SADVLAQVLH TNAQRLARLT HSKQWIGSAM
AGCPGMMGCN
  HMGRclustalW{archaeoglo} .....GEEVV EGIMLAYAFA AADPFRCATH NKGIMNGISA
LM.....
  HMGRclustalW{pseudomonas} TAEFSGEAVI EGILDAYAFA AVDPYRAATH NKGIMNGIDP
LI.....

Consensus GKSIVCEAVI PAEVRKVLK TTVEALVELN ILKQLVGSAM AG--
SLGGFN

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K

FIG. 32NN

1000

951

HMGRclustalW{methanobac}	AHYANIIGAI FLATGQDEAH IVEGSLGVTI AEERK.....
.....GDLYF	
HMGRclustalW{methanococ}	AHYANIIGAI FLATGQDEAH IVEGSLGITM AEVED.....
.....DGLYF	
HMGRclustalW{halobacter}	AHVANVVAAM FLATGQDEAQ VVEGANAITT AEVQD.....
.....GDLYV	
HMGRclustalW{sulfolobus}	AHFANIVTAI FIATGQDVAQ IVESSSGYTW TEVRG.....
.....EDLYI	
HMGRclustalW{ yeast2}	AHAANLVTAL FLALGQDPAQ NVESSNCITL MKEVD.....
.....GDLRI	
HMGRclustalW{ yeast1}	AHAANLVTAV FLALGQDPAQ NVESSNCITL MKEVD.....
.....GDLRI	
HMGRclustalW{phycomycs}
.....	
HMGRclustalW{ fusarium}	AHAANIVAAI FLATGQDPAQ VVESANCITI MKNLN.....
.....GALQI	
HMGRclustalW{ candida}	AQAANMVTAV YLALGQDPAQ NVESSNCITL MTETED....
.....GDLKV	
HMGRclustalW{dictyoste2}	AHASNIVTAL YIATGQDPAQ NVESSNCITL MESINGG...
.....KDLVI	
HMGRclustalW{wheat1}	AHASNIATAT FIATGQDPAQ NVESSQCITM LEAVNEG...
.....KDLHI	
HMGRclustalW{ rice}	AHASNIVTAL FIATGQDPAQ NVESSQCITM LEEVNDG...
.....DDLHI	
HMGRclustalW{ corn}	AHASNIVTAI FIATGQDPAQ NVESSHCITM LEPVNAG...
.....RDLHI	
HMGRclustalW{wheat3}	AHASNIVTAI FIATGQDPAQ NVESSQCITM LEAVNDG...
.....KDLHI	
HMGRclustalW{wheat2}	AHASNIVSAI FIATGQDPAQ NVESSQCITM LEAVNGG...
.....RDLHI	
HMGRclustalW{ soybean}	AHASNIVSAI FIATGQDPAQ NVESSHCITM MEAVNDG...
.....RDLHI	
HMGRclustalW{rubbertre3}	AHASNMVTAV YIATGQDPAQ NVESSHCITM MEAVNDG...
.....KDLHI	
HMGRclustalW{rosyperiwi}	AHASNIVSAI FIATGQDPAQ NVESSQCITM MEAVNDG...
.....KDLHI	
HMGRclustalW{ tomato}	AHASNIVSAV FIATGQDPAQ NIESSHCITM MEAVNDG...
.....KDLHI	
HMGRclustalW{woodtobacc}	AHASNIVSAV YIATGQDPAQ NIESSHCITM MEAVNDG...
.....KDLHV	
HMGRclustalW{ potato}	AHASNIVSAV YLATGQDPAQ NVESSHCITM MEAVNDG...
.....KDLHV	
HMGRclustalW{radish}	RHASNIVSAV FLATGQDPAQ NVESSQCITM MEAVNDG...
.....KDIHI	
HMGRclustalW{arabadosis1}	AHASNIVSAV FIATGQDPAQ NVESSQCITM MEAVNDG...
.....KDIHI	
HMGRclustalW{cucumismel}	AHSSNIVSAI FLATGQDPAQ NVESSHCITM MEPVNNG...
.....RDLHI	
HMGRclustalW{rubbertre2}	AHAGNIVSAI FIATGQDPAQ NVESSHCITM MEAVNDG...
.....KDLHI	
HMGRclustalW{rubbertre1}	AHAGNIVSAI FIATGQDPAQ NVESSHCITM MEAVNDG...
.....KDLHI	
HMGRclustalW{camptothec}	AHASNIVSAV YLATGQDPAQ NVESSHCITM MEAVNDG...
.....KDLHV	
HMGRclustalW{arabados2}	AHSSNIVSAV FIATGQDPAQ NVESSHCITM ILPDGD....
.....DLHI	
HMGRclustalW{chineseham}	AHAANIVTAI YIACGQDAAQ NVGSSNCITL MEASGPTN..

FIG. 3200

```

.....EDLYI
  HMGRclustalW(chineseha2} AHAANIVTAI YIACGQDAAQ NVGSSNCITL MEASGPTN..
.....EDLYI
  HMGRclustalW(syrianhamst} AHAANIVTAI YIACGQDAAQ NVGSSNCITL MEASGPTN..
.....EDLYI
    HMGRclustalW(      rat} LHAANIVTAI YIACGQDAAQ NVGSSNCITL MEASGPTN..
.....EDLYI
    HMGRclustalW(      rabbit} AHAANYVTAI YIACGQDAAQ NVGSSNCITL MEASGPPN..
.....EDLYI
    HMGRclustalW(      human} AHAANIVTAI YIACGQDAAQ NVGSSNCITL MEASGPTN..
.....EDLYI
    HMGRclustalW(      mouse} AHAANIVTAI YIACGQDAAQ NVGSSNCITL MEASGPTN..
.....EDLYI
    HMGRclustalW(      xenopus} AHAANIVTAI YIACGQDAAQ NVGSSNCITI MEATGPTY..
.....EDLYI
    HMGRclustalW(sea urchin} AHAANIVTAI YIATGQDAAQ NIASSNCMTL METRGPKG..
.....GDLYL
    HMGRclustalW( cockroach} AHAANIVTAI FIATGQDPAQ NVGSSNCMTL MEPWGEDG..
.....KDLV
    HMGRclustalW(drosophila} AHAANMVTAV FLATGQDPAQ NVTSSNCSTA MECWAENS..
.....EDLYM
    HMGRclustalW(dictyostel} AFASNIVTAI FLATGQDCAQ NVESSNCITQ MEACNDG...
.....QDLVI
    HMGRclustalW(schistosom} AHAANIIAGM FAATGQDLAQ VVDSSSCLTQ LEVDLSD...
.....DSLVA
    HMGRclustalW(archaeoglo} ..... .IATGNDFRA IEAGAHSYAA IGG.YKPLTT
YEVDRKGNLV
    HMGRclustalW(pseudomonas} ..... .VATGNDWRA VEAGAHAYAC RSGHYGSLTT
WEKDNNGHLV

Consensus AHAANIVTAI FIATGQDPAQ NVESSNCITM MEAVNDGN-- -----
KDLHI

```

D

FIG. 32PP

1050	1001
HMGRclustalW{methanobac}	AVNLPDVPLA TVGGGTGLET ASECLDIMGV RGGG.....
RVHFAEIVG	
HMGRclustalW{methanococ}	SVTLPDVPIG TVGGGTRVET QKECLEMLGC YGDN.....
KALKFAEIVG	
HMGRclustalW{halobacter}	SVSIASLEVG TVGGGTLPT QSEGLDILGV SGGGDP.AGS
NADALAECIA	
HMGRclustalW{sulfolobus}	SVTLPSLEVG TVGGGTRLPT QKEALSIMGV YGSGNP.PGS
NAKCLAEIIA	
HMGRclustalW{ yeast2}	SVSMPSIEVG TIGGGTVLEP QGAMLDLLGV RGPHPTEPGA
NARQLARIIA	
HMGRclustalW{ yeast1}	SVSMPSIEVG TIGGGTVLEP QGAMLDLLGV RGPHTAPGT
NARQLARIVA	
HMGRclustalW{phycomycetes}
.....	
HMGRclustalW{ fusarium}	SVSMPSLEVG TLGGGTILEP QGAMLDILGV RGSHTPNPGD
NARRLARIIG	
HMGRclustalW{ candida}	SVSMPSIEVG TIGGGTILDP QGSMLLELLGV RG.PADVPGA
NARQLAKIVA	
HMGRclustalW{dictyoste2}	SVTMPSIEVG TVGGGTHLPA QSACLDLLKI RGANLERPGA
NSEQLARVVA	
HMGRclustalW{wheat1}	SVTMPPIEV.
.....	
HMGRclustalW{ rice}	SVTMPSIEVG TIGGGTCLAS QAACLNLLGV KGSNHEGSPGA
NAGRLATIVA	
HMGRclustalW{ corn}	SVTMPSIEVG TVGGGTQLAS QSACLDLLGV RGASFDRPGS
NARLLATVVA	
HMGRclustalW{wheat3}	SVTMPPIEV.
.....	
HMGRclustalW{wheat2}	SVTMPPIEV.
.....	
HMGRclustalW{ soybean}	SVTMPSIEVG TVGGGTQLAS QSACLNLLGV KGASKESPGS
NSRLLATIVA	
HMGRclustalW{rubbertre3}	SVSMPSIEVG TVGGGTQLAS QSACLNLLGV KGASKDSPGS
NSRLLATIVA	
HMGRclustalW{rosyperiwi}	SVTMPSIEVG TVGGGTQLAS QSACLNLLGV KGASKDSPGA
NSRLLATIVA	
HMGRclustalW{ tomato}	SVTMPSIEVG TVGGGTQLAS QSACLNLLGV KGANREAPGS
NARLLATVVA	
HMGRclustalW{woodtobacc}	SVTMPSIEVG TVGGGTQLAS QSACLNLLGV KGANREVPGS
NARLLATIVA	
HMGRclustalW{ potato}	SVTMPSIEVG TVGGGTQLAS QSACLNLLGV KGANRDAPGS
NARLLATIVA	
HMGRclustalW{radish}	SVTMPSIEVG TVGGGTQLAS QSACLNLLGV KGASKESPGM
NSRLLATIVA	
HMGRclustalW{arabidopsis1}	SVTMPSIEVG TVGGGTQLAS QSACLNLLGV KGASTESPGM
NARLLATIVA	
HMGRclustalW{cucumismel}	SVTMPSIEVG TVGGGTQLAS QSACLNLLGV KGASKESPGA
NSRLLATIVA	
HMGRclustalW{rubbertre2}	SVTLPSIEVG TVGGGTQLAS QSACLNLLGV MGACKESPGS
YSRLLATIVA	
HMGRclustalW{rubbertrel}	SVTMPSIEVG TVGGGTQLAS QSACLNLLGV KGANKESPGS
NSRLLAIVA	
HMGRclustalW{camptothec}	SVTMPSIEVG TVGGGTQLAS QSACLNLLGV KGASKEAPGS
NARLLATIVA	
HMGRclustalW{arabidops2}	SVSMPCIEVG TVGGGTQLAS QAACLNLLGV KGSNNEKPGS
NAQQLARIVA	
HMGRclustalW{chineseham}	SCTMPSIEIG TVGGGTNLLP QQACLQMLGV QGACKDNPGA
NARQLARIVC	

FIG. 32QQ

HMGRclustalW{chineseha2}	SCTMPSIEIG	TVGGGTNLLP	QQACLQMLGV	QGACKDNPGZ
NARQLARIVC				
HMGRclustalW{syrianhamst}	SCTMPSIEIG	TVGGGTNLLP	QQACLQMLGV	QGACKDNPGZ
NARQLARIVC				
HMGRclustalW{rat}	SCTMPSIEIG	TVGGGTNLLP	QQACLQMLGV	QGACKDNPGZ
NARQLARIVC				
HMGRclustalW{rabbit}	SCTMPSIEIG	TVGGGTNLLP	QQACLQMLGV	QGACKDSPGE
NARQLARIVC				
HMGRclustalW{human}	SCTMPSIEIG	TVGGGTNLLP	QQACLQMLGV	QGACKDNPGZ
NARQLARIVC				
HMGRclustalW{mouse}	SCTMPSIEIG	TVGGGTNLLP	QQACLQMLGV	QGACKDNPGZ
NARQLARIVC				
HMGRclustalW{xenopus}	SCTMPSIEIG	TVGGGTNLAP	QQACLQMLGV	QGASTETPGK
NACQLAQIVC				
HMGRclustalW{sea urchin}	SCTMPSIELG	TVGGGTVLPP	QSACLQMLGV	KGSNIHGSGI
NASQLARIVC				
HMGRclustalW{cockroach}	SCTMPSIEIG	TIGGGTVLPP	QAACLDMLGV	RGANEMCPGE
NANTLARIVC				
HMGRclustalW{drosophila}	TCTMPSLEVG	TVGGGTGLPG	QSACLEMLGV	RGAEATRPGD
NAKQLAQIVC				
HMGRclustalW{dictyostel}	TVTMPSEIEG	TVGGGTSLPA	QSACLDIIGV	KGSSSSKPGA
NADQLAKTIA				
HMGRclustalW{schistosom}	SVTMPCLEVG	TVGGGTRLTG	QRACLDLLDL	SV.....D.R
PTEHLSRIIA				
HMGRclustalW{archaeoglo}	GTIEIPMAVG	VIGGATKVP	LAKISLKITG	VNTAEELARV
AAAL				
HMGRclustalW{pseudomonas}	GTLEMPMPVG	LVGGATKTHP	LAQLSLRILG	VKTAQALAEI
AVAV				
Consensus	SVTMPSEIEG	TVGGGTQLAP	QSACLNLLGV	KGA-KESPGS
NARQLARIVA				

NADH binding domain 2

FIG. 32RR

	1051
1100	
HMGRclustalw{methanobac}	GAVLAGELSL MGALAAGHLA RAHSELGRG.
.....	
HMGRclustalw{methanococ}	AAVLAGESSL LGALAAGHLG KAHQELGR..
.....	
HMGRclustalw{halobacter}	VGSLAGESSL LSALASRHLS SAHAELGR..
.....	
HMGRclustalw{sulfolobus}	STVLSGELNL LAALSNKELG KAHAKLGRAM KV.....
.....	
HMGRclustalw{ yeast2}	CAVLAGESSL CSALAAGHLV QSEMTENRK. ..TNKANELP
QPS.....	
HMGRclustalw{ yeast1}	CAVLAGESSL CAALAAGHLV QSEMTENRKP AEPTKPNLD
ATDI.....	
HMGRclustalw{phycomyces}
.....	
HMGRclustalw{ fusarium}	AAVLAGESSL CSALAAGHLV RAHMQHNRSA APSRSTTPGS
SHDARLTGHD	
HMGRclustalw{ candida}	SIVLSGELSL VSALAAGHLV QSHMQHNRAA AKK.....
.....	
HMGRclustalw{dictyoste2}	AAVLAGESSL MSALAAGHLV RSHLKHNRTK EAPAPQADTI
SMTHNLPHSD	
HMGRclustalw{wheat1}
.....	
HMGRclustalw{ rice}	GSVVAGRALL LAALASGHLV KSEMMYNRSS KDVAK.....
.....	
HMGRclustalw{ corn}	GGVLAGESSL LSALAAGQLV KSEMKYNRSS KDVSS.....
.....	
HMGRclustalw{wheat3}
.....	
HMGRclustalw{wheat2}
.....	
HMGRclustalw{ soybean}	GSVLAGESSL MSAIAAGQLV NSHMKYNRSS KDVTX.....
.....	
HMGRclustalw{rubbertre3}	GSVLAGESSL MSAIAAGQLV NSHMKYNRSA KDVSK.....
.....	
HMGRclustalw{rosyperiwi}	GSVLAGESSL MSAISAGQLV RSEMKYNRSS KDITN.....
.....	
HMGRclustalw{ tomato}	GSVLAGESSL MSAISSGQLV NSHMKYNRST KDVTX.....
.....	
HMGRclustalw{woodtobacc}	GSVLAGESSL MSAISAGQLV KSHMKYNRST KDVTX.....
.....	
HMGRclustalw{ potato}	GSVLAGESSL MSAISAGQLV KSHMKYNRSI KDISK.....
.....	
HMGRclustalw{radish}	GAVLAGELSL MSAIAAGQLV RSEMKYNRSS RDISG.....
.....	
HMGRclustalw{arabadosis1}	GAVLAGELSL MSAIAAGQLV RSEMKYNRSS RDISG.....
.....	
HMGRclustalw{cucumismel}	GSVLAGESSL MSAIAAGQLV RSEMKYNRSS RDVSK.....
.....	
HMGRclustalw{rubbertre2}	GSVLAGESSL MSAIAAGQLV KSEMKYNRSS KDVSK.....
.....	
HMGRclustalw{rubbertrel}	GSVLAGESSL MSAIAAGQLV KSEMKYNRSS KDMSK.....
.....	
HMGRclustalw{camptothec}	GSVLAGESSL MSAIAAGQLV NSHMKYNRSN KDVTX.....
.....	
HMGRclustalw{arabados2}	GSVLAGESSL MSAIAAGQLV KSEMKYNRSS RDIGP.....
.....	
HMGRclustalw{chineseham}	GTVMAGESSL MAALAAGHLV RSEMVENRSK INLQD.....

FIG. 32SS

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.....
HMGRclustalW(chineseha2} GTVMAGELSL MAALAAGHLV RSEMVENRSK INLQD.....
.....
HMGRclustalW(syrianhamst} GTVMAGELSL MAALAAGHLV RSEMVENRSK INLQD.....
.....
HMGRclustalW( rat} GTVMAGELSL MAALAAGHLV RSEMVENRSK INLQD.....
.....
HMGRclustalW( rabbit} GTVMAGELSL MAALAAGHLV KSHMIHNRSK INLQD.....
.....
HMGRclustalW( human} GTVMAGELSL MAALAAGHLV KSHMIHNRSK INLQD.....
.....
HMGRclustalW( mouse} GTVMAGELSL MAALAAGHLV RSEMVENRSK INLQD.....
.....
HMGRclustalW( xenopus} STVMAGELSL MAALAAGHLV KSEMVENRSK INLQD.....
.....
HMGRclustalW(sea urchin} ATVMAGELSL MSALAAGHLV KSEMKENRSA LNIASPLPSI
DEVATHRRSK
HMGRclustalW( cockroach} GTVLAGELSL MSALAAGHLV KSEMRHNRSS VSTSG.....
.....
HMGRclustalW(drosophila} ATVMAGELSL MAALVNSDLV KSEMRHNRSS IAVNSAN...
.....
HMGRclustalW(dictyostel} SAVMAGELSL MSALSAGHLM KSHLQYNRAK TN.....
.....
HMGRclustalW(schistosom} GTVLAAELSL MAALDTDDL V KAHMHFNRAK QSTNSHSCSH
STTTDNNDNI
HMGRclustalW(archaeoglo} ..GLAQNFPA LRALATEGIQ RGHMELHARN LAIMAGATGD
EVDVVVEIMV
HMGRclustalW(pseudomonas} ..GLAQNLGA MRALATEGIQ RGHMALHARN IAVVAGARGD
EVDWVARQLV

Consensus GTVLAGELSL MSALAAGHLV KSEMK-NRSS KDVSK-----
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* † ‡

FIG. 32TT

1152	1101
HMGRclustalW{methanobac}
HMGRclustalW{methanococ}
HMGRclustalW{halobacter}
HMGRclustalW{sulfolobus}
HMGRclustalW{ yeast2}NKGPPCKT SALL.....
HMGRclustalW{ yeast1}NRLKDGSV TCIKS.....
HMGRclustalW{phycomyces}
HMGRclustalW{ fusarium}	QCPRALSVNN VDERRRYSEV KAIDE.....
HMGRclustalW{ candida}
HMGRclustalW{dictyoste2}
HMGRclustalW{wheat1}
HMGRclustalW{ rice}AAS.....
HMGRclustalW{ corn}TTATEK TRQREVDV..
HMGRclustalW{wheat3}
HMGRclustalW{wheat2}
HMGRclustalW{ soybean}IS.....
HMGRclustalW{rubbertre3}ITF.....
HMGRclustalW{rosyperiwi}IASSQL ESDS.....
HMGRclustalW{ tomato}ASS.....
HMGRclustalW{woodtobacc}ASS.....
HMGRclustalW{ potato}
HMGRclustalW{radish}ATTTT.....
HMGRclustalW{arabadopsis1}ATTTTT TTT.....
HMGRclustalW{cucumismel}LES.....
HMGRclustalW{rubbertre2}AAS.....
HMGRclustalW{rubbertrel}AAS.....
HMGRclustalW{camptothec}ASS.....
HMGRclustalW{arabadops2}SSQVNR.....
HMGRclustalW{chineseham}LQGTCTK KSA.....

FIG. 32UU

```

HMGRclustalW{chineseha2} ..... ..LQGTCTK KSA.....
.....
HMGRclustalW{syrianhamst} ..... ..LQGTCTK KAA.....
.....
HMGRclustalW{      rat} ..... ..LQGTCTK KAA.....
.....
HMGRclustalW{      rabbit} ..... ..LEGACTK KAA.....
.....
HMGRclustalW{      human} ..... ..LQGTCTK KTA.....
.....
HMGRclustalW{      mouse} ..... ..LQGTCTK KAA.....
.....
HMGRclustalW{      xenopus} ..... ..LPGTCTK KAA.....
.....
HMGRclustalW{sea urchin} SVDFSALKES SAAAPGTCTA NAS.....
.....
HMGRclustalW{ cockroach} .....S ...EPSTPAC KS.....
.....
HMGRclustalW{drosophila} .....NP LNVTVSSCST IS.....
.....
HMGRclustalW{dictyostel} .....
.....
HMGRclustalW{schistosom} SNIYDNENVA LSSKIPVTDN SDIRESVHSL HVKPFPPVKS
LSVNPEISHY TM
HMGRclustalW{archaeoglo} RDGKIRLDYA KEVLRLRS. ....
.....
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.....
Consensus -----A ----LQGTCTK KAA-----
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SEQUENCE LISTING

<110> Monsanto Company

<120> TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROID COMPOUNDS

<130>- MTC6783.3

<160> 33

<170> PatentIn version 3.0

<210> 1

<211> 585

<212> PRT

<213> Arabidopsis thaliana

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Leu Ser Thr Arg Arg Phe Thr Thr Gly Ala Thr Tyr Ile Arg Arg Trp
          35           40           45
Lys Ala Thr Ala Ala Gln Thr Leu Lys Leu Ser Ala Val Asn Ser Thr
          50           55           60
Val Met Met Lys Pro Ala Lys Ile Ala Leu Asp Gln Phe Ile Ala Ser
65           70           75           80
Leu Phe Thr Phe Leu Leu Leu Tyr Ile Leu Arg Arg Ser Ser Asn Lys
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Asn Lys Lys Asn Arg Gly Leu Val Val Ser Gln Asn Asp Thr Val Ser
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          115          120          125
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          130          135          140
Gly Arg Arg Val His Val Ile Glu Arg Asp Phe Ser Glu Gln Asp Arg
145          150          155          160
Ile Val Gly Glu Leu Leu Gln Pro Gly Gly Tyr Leu Lys Leu Ile Glu
          165          170          175
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Gly Tyr Val Leu Phe Lys Asp Gly Lys His Thr Lys Leu Ala Tyr Pro
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 225 230 235 240
 Arg Leu Glu Gln Gly Thr Val Thr Ser Leu Leu Glu Glu His Gly Thr
 245 250 255
 Ile Lys Gly Val Arg Tyr Arg Thr Lys Glu Gly Asn Glu Phe Arg Ser
 260 265 270
 Phe Ala Pro Leu Thr Ile Val Cys Asp Gly Cys Phe Ser Asn Leu Arg
 275 280 285
 Arg Ser Leu Cys Lys Pro Lys Val Asp Val Pro Ser Thr Phe Val Gly
 290 295 300
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 Val Leu Gly Asp Pro Ser Pro Ile Leu Met Tyr Pro Ile Ser Ser Ser
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 465 470 475 480
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 Ile Tyr Ala Val Cys Arg Leu Met Leu Pro Phe Pro Ser Ile Glu Ser
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 gacgttatca tcgttggggc tggagtaggc ggctcggctc tcgcatatgc tcttgctaag 240
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<213> Arabidopsis thaliana

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          20           25           30
Thr Val Phe Tyr Val Thr Asn Arg Gly Lys Lys Ala Thr Gln Leu Ala
          35           40           45
Asp Ala Val Val Glu Glu Arg Glu Asp Gly Ala Thr Asp Val Ile Ile
          50           55           60
Val Gly Ala Gly Val Gly Gly Ser Ala Leu Ala Tyr Ala Leu Ala Lys
65           70           75           80
Asp Gly Arg Arg Val His Val Ile Glu Arg Asp Leu Arg Glu Pro Glu
          85           90           95
Arg Ile Met Gly Glu Phe Met Gln Pro Gly Gly Arg Leu Met Leu Ser
          100          105          110
Lys Leu Gly Leu Glu Asp Cys Leu Glu Gly Ile Asp Ala Gln Lys Ala
          115          120          125
Thr Gly Met Thr Val Tyr Lys Asp Gly Lys Glu Ala Val Ala Ser Phe
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 Lys Gly Val Ile Lys Gly Val Thr Tyr Lys Asn Ser Ala Gly Glu Glu
 195 200 205
 Thr Thr Ala Leu Ala Pro Leu Thr Val Val Cys Asp Gly Cys Tyr Ser
 210 215 220
 Asn Leu Arg Arg Ser Leu Asn Asp Asn Asn Ala Glu Val Leu Ser Tyr
 225 230 235 240
 Gln Val Gly Phe Ile Ser Lys Asn Cys Gln Leu Glu Glu Pro Glu Lys
 245 250 255
 Leu Lys Leu Ile Met Ser Lys Pro Ser Phe Thr Met Leu Tyr Gln Ile
 260 265 270
 Ser Ser Thr Asp Val Arg Cys Val Phe Glu Val Leu Pro Asn Asn Ile
 275 280 285
 Pro Ser Ile Ser Asn Gly Glu Met Ala Thr Phe Val Lys Asn Thr Ile
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 Ala Pro Gln Val Pro Leu Lys Leu Arg Lys Ile Phe Leu Lys Gly Ile
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 Thr Leu Ser Glu Lys Lys Gly Val Ile Leu Leu Gly Asp Ala Phe Asn
 340 345 350
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 355 360 365
 Ile Leu Ile Leu Arg Arg Leu Leu Gln Pro Leu Ser Asn Leu Gly Asn
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 Ala Gln Lys Ile Ser Gln Val Ile Lys Ser Phe Tyr Asp Ile Arg Lys
 385 390 395 400
 Pro Met Ser Ala Thr Val Asn Thr Leu Gly Asn Ala Phe Ser Gln Val
 405 410 415
 Leu Val Ala Ser Thr Asp Glu Ala Lys Glu Ala Met Arg Gln Gly Cys
 420 425 430
 Tyr Asp Tyr Leu Ser Ser Gly Gly Phe Arg Thr Ser Gly Met Met Ala
 435 440 445

Leu Leu Gly Gly Met Asn Pro Arg Pro Ile Ser Leu Ile Tyr His Leu
 450 455 460
 Cys Ala Ile Thr Leu Ser Ser Ile Gly His Leu Leu Ser Pro Phe Pro
 465 470 475 480
 Ser Pro Leu Gly Ile Trp His Ser Leu Arg Leu Phe Gly Leu Ala Met
 485 490 495
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 Ala Leu
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<212> PRT

<213> Arabidopsis thaliana

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Leu Ala Asp Thr Val Ala Glu Asp Gln Lys Asp Gly Ala Ala Asp Val
35 40 45
Ile Ile Val Gly Ala Gly Val Gly Gly Ser Ala Leu Ala Tyr Ala Leu
50 55 60
Ala Lys Asp Gly Arg Arg Val His Val Ile Glu Arg Asp Met Arg Glu
65 70 75 80

3NSDOCID: <WO 02061072A2_1_>

10

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405 410 415

Gln Gly Val Tyr Asp Tyr Leu Cys Ser Gly Gly Phe Arg Thr Ser Gly
420 425 430

Met Met Ala Leu Leu Gly Gly Met Asn Pro Arg Pro Leu Ser Leu Val
435 440 445

Tyr His Leu Cys Ala Ile Thr Leu Ser Ser Ile Gly Gln Leu Leu Ser
450 455 460

Pro Phe Pro Ser Pro Leu Arg Ile Trp His Ser Leu Lys Leu Phe Gly
465 470 475 480

Leu Ala Met Lys Met Leu Val Pro Asn Leu Lys Ala Glu Gly Val Ser
485 490 495

Gln Met Leu Phe Pro Ala Asn Ala Ala Ala Tyr His Lys Ser Tyr Met
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Ala Ala Thr Thr Leu
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<211> 392

<212> DNA

<213> Arabidopsis thaliana

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<212> PRT

<213> Arabidopsis thaliana

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Leu Ala Asp Thr Val Ala Glu Asp Gln Lys Asp Gly Ala Ala Asp Val	35	40	45
Ile Ile Val Gly Ala Gly Val Gly Gly Ser Ala Leu Ala Tyr Ala Leu	50	55	60
Leu Ser Val Arg Leu Glu Glu Gly Thr Val Lys Ser Leu Leu Glu Glu	65	70	75
Lys Gly Val Val Lys Gly Val Thr Tyr Lys Asn Lys Glu Cys Glu Gln	85	90	95
Thr Thr Ala Leu Ala Pro Leu Thr Val Val Cys Asp Gly Cys	100	105	110

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<223> X=any amino acid

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 Arg His Asp Arg Lys Thr Val Ser Thr Val Thr Ser Asp Val Gly Ser
 50 55 60
 Val Asn Ile Thr Gly Asp Thr Val Ala Asp Val Ile Val Val Gly Ala
 65 70 75 80
 Gly Val Ala Gly Ser Ala Leu Ala Tyr Thr Leu Gly Lys Gly Lys Phe
 85 90 95
 Lys Arg Arg Val His Val Ile Glu Arg Asp Leu Ser Glu Pro Asp Arg
 100 105 110
 Ile Val Gly Glu Leu Leu Gln Pro Xaa Gly Tyr Leu Lys Leu Leu Glu
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gatcttactg ctgagaacag tacacagtga tttcacctg acaactcgag aaggaaagca    1140
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tgagcttgag ttagtgtcac ctttccctga aatcaactgg aatgctttgg tcgttggtgc    1440
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<210> 13

<211> 473

<212> PRT

<213> Arabidopsis thaliana

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20           25           30
Lys Thr Ser Val Val Pro Leu Pro Pro Val Leu Gln Ala Trp Pro Pro
35           40           45
Phe Ile Gly Ser Leu Ile Arg Phe Met Lys Gly Pro Ile Val Leu Leu
50           55           60
Arg Glu Glu Tyr Pro Lys Leu Gly Ser Val Phe Thr Val Lys Leu Leu
65           70           75           80

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Phe	Asn	Ala	Tyr	Glu	Ser	Glu	Leu	Ser	Gln	Lys	Glu	Ile	Tyr	Lys	Phe
			100					105					110		
Asn	Val	Pro	Thr	Phe	Gly	Pro	Gly	Val	Val	Phe	Asp	Val	Asp	Tyr	Pro
		115					120					125			
Val	Arg	Met	Glu	Gln	Phe	Arg	Phe	Phe	Ser	Ser	Ala	Leu	Lys	Asp	Tyr
	130					135					140				
Phe	Ser	Lys	Trp	Gly	Glu	Ser	Gly	Glu	Val	Asp	Leu	Lys	Ala	Glu	Leu
145					150					155					160
Glu	Arg	Leu	Ile	Thr	Leu	Thr	Ala	Ser	Arg	Cys	Leu	Leu	Gly	Arg	Glu
				165					170					175	
Val	Arg	Asp	Gln	Leu	Phe	Asp	Asp	Val	Ala	Pro	Leu	Phe	His	Asp	Leu
			180					185					190		
Asp	Lys	Gly	Met	Gln	Pro	Ile	Ser	Val	Ile	Phe	Pro	Lys	Leu	Pro	Ile
		195					200					205			
Pro	Ala	His	Asn	Cys	Arg	Asp	Arg	Ala	Arg	Gly	Lys	Ile	Ala	Lys	Ile
	210					215					220				
Phe	Ser	Asn	Ile	Ile	Ala	Thr	Arg	Lys	Arg	Ser	Gly	Asp	Lys	Ser	Glu
225					230					235					240
Asn	Asp	Met	Leu	Gln	Cys	Phe	Ile	Asp	Ser	Lys	Tyr	Lys	Asp	Gly	Arg
				245					250					255	
Glu	Thr	Thr	Glu	Ser	Glu	Val	Thr	Gly	Leu	Leu	Ile	Ala	Gly	Leu	Phe
			260					265					270		
Ala	Gly	Gln	His	Thr	Ser	Ser	Ile	Thr	Ala	Thr	Trp	Thr	Gly	Ala	Tyr
		275					280					285			
Leu	Ile	Gln	Asn	Lys	His	Trp	Trp	Ser	Ala	Ala	Leu	Asp	Glu	Gln	Lys
	290					295					300				
Lys	Leu	Ile	Gly	Lys	His	Gly	Asp	Lys	Ile	Asp	Tyr	Asp	Val	Leu	Ser
305					310					315					320
Glu	Met	Asp	Phe	Leu	Phe	Arg	Ser	Ala	Lys	Glu	Ala	Leu	Arg	Leu	His
				325					330					335	
Pro	Pro	Lys	Ile	Leu	Leu	Leu	Arg	Thr	Val	His	Ser	Asp	Phe	Thr	Val
			340					345					350		
Thr	Thr	Arg	Glu	Gly	Lys	Gln	Tyr	Glu	Ile	Pro	Lys	Gly	His	Ile	Val
		355					360					365			
Ala	Thr	Ser	Pro	Ala	Phe	Ala	Asn	Arg	Leu	Pro	His	Val	Tyr	Lys	Asp
	370					375					380				

15

Pro Glu Asn Phe Asp Pro Asp Arg Phe Ser Lys Glu Arg Glu Glu Asp
385 390 395 400

Lys Ala Ala Gly Ser Cys Ser Tyr Ile Ser Leu Gly Ala Gly Arg His
405 410 415

Glu Cys Pro Gly Gly Ser Phe Ala Phe Leu Gln Ile Lys Ala Val Trp
420 425 430

Cys His Leu Leu Arg Asn Phe Glu Leu Glu Leu Val Ser Pro Phe Pro
435 440 445

Glu Ile Asn Trp Asn Ala Leu Val Val Gly Ala Lys Gly Asn Val Met
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Val Arg Tyr Lys Arg Arg Pro Phe Ser
465 470

<210> 14

<211> 523

<212> DNA

<213> Arabidopsis thaliana

<400> 14

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aagcttctga atctgatctt agtcagcagg aagtgtatca gttcaatgtc cctacttttg      180
gtcctggagt tgttttcgat gttgattatt ctgtttcgtc aggagcagtt cggttcttca     240
ctgaggcact tagagttaac aagttgaagg gttatgtgga tatgatgggtt actgaagctg     300
aggattactt ctctaaatgg ggagagagtg gtgaagttga tattaagggtt gagctagaga     360
ggctcatcat cttgactgca agtgatgttt actgggtcga gaagttcgtg atcagctttt      420
tgatgatgtc tctgctttgt tccatgacct tgacaatgga atgcttccca tcagtgttc       480
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<212> PRT

<213> Arabidopsis thaliana

<400> 15

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Glu Val Ser Ala His Phe Phe Lys Ala Ser Glu Ser Asp Leu Ser Gln

16

35

40

45

Gln Glu Val Tyr Gln Phe Asn Val Pro Thr Phe Gly Pro Gly Val Val
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Phe Asp Val Asp Tyr Ser Val Arg Gln Glu Gln Phe Gly Ser Ser Leu
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Arg His Leu Glu Leu Thr Ser
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<210> 16

<211> 1852

<212> DNA

<213> Arabidopsis thaliana

<400> 16

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ccaaattgaa aaacaatgga attggattcg gagaacaaat tgttgaagac gggtttggtt      240
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aagaagcgtc ttcctcctac tcttaaagct tggcctccat tggttggaag tcttatcaaa      360
ttcttgaaag gacctattat tatgcttaga gaggaatacc ctaagcttgg aagtgtgttt      420
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gatgagcaga agaacctgat tgcgaaacat ggagacaaga tcgatcatga tatcttatcc     1200

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17

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<210> 17
 <211> 488
 <212> PRT
 <213> Arabidopsis thaliana

<400> 17

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Asp	Ser	Lys	Lys	Lys	Arg	Leu	Pro	Pro	Thr	Leu	Lys	Ala	Trp	Pro	Pro	35	40	45	
Leu	Val	Gly	Ser	Leu	Ile	Lys	Phe	Leu	Lys	Gly	Pro	Ile	Ile	Met	Leu	50	55	60	
Arg	Glu	Glu	Tyr	Pro	Lys	Leu	Gly	Ser	Val	Phe	Thr	Val	Asn	Leu	Val	65	70	75	80
His	Lys	Lys	Ile	Thr	Phe	Leu	Ile	Gly	Pro	Glu	Val	Ser	Ala	His	Phe	85	90	95	
Phe	Lys	Ala	Ser	Glu	Ser	Asp	Leu	Ser	Gln	Gln	Glu	Val	Tyr	Gln	Phe	100	105	110	
Asn	Val	Pro	Thr	Phe	Gly	Pro	Gly	Val	Val	Phe	Asp	Val	Asp	Tyr	Ser	115	120	125	
Val	Arg	Gln	Glu	Gln	Phe	Arg	Phe	Phe	Thr	Glu	Ala	Leu	Arg	Val	Asn	130	135	140	

Lys Leu Lys Gly Tyr Val Asp Met Met Val Thr Glu Ala Glu Asp Tyr
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 Phe Ser Lys Trp Gly Glu Ser Gly Glu Val Asp Ile Lys Val Glu Leu
 165 170 175
 Glu Arg Leu Ile Ile Leu Thr Ala Ser Arg Cys Leu Leu Gly Arg Glu
 180 185 190
 Val Arg Asp Gln Leu Phe Asp Asp Val Ser Ala Leu Phe His Asp Leu
 195 200 205
 Asp Asn Gly Met Leu Pro Ile Ser Val Leu Phe Pro Tyr Leu Pro Ile
 210 215 220
 Pro Ala His Arg Arg Arg Asp Arg Ala Arg Glu Lys Leu Ser Glu Ile
 225 230 235 240
 Phe Ala Lys Ile Ile Gly Ser Arg Lys Arg Ser Gly Lys Thr Glu Asn
 245 250 255
 Asp Met Leu Gln Cys Phe Ile Glu Ser Lys Tyr Lys Asp Gly Arg Gln
 260 265 270
 Thr Thr Glu Ser Glu Val Thr Gly Leu Leu Ile Ala Ala Leu Phe Ala
 275 280 285
 Gly Gln His Thr Ser Ser Ile Thr Ser Thr Trp Thr Gly Ala Tyr Leu
 290 295 300
 Met Arg Tyr Lys Glu Tyr Phe Ser Ala Ala Leu Asp Glu Gln Lys Asn
 305 310 315 320
 Leu Ile Ala Lys His Gly Asp Lys Ile Asp His Asp Ile Leu Ser Glu
 325 330 335
 Met Asp Val Leu Tyr Arg Cys Ile Lys Glu Ala Leu Arg Leu His Pro
 340 345 350
 Pro Leu Ile Met Leu Met Arg Ala Ser His Ser Asp Phe Ser Val Thr
 355 360 365
 Ala Arg Asp Gly Lys Thr Tyr Asp Ile Pro Lys Gly His Ile Val Ala
 370 375 380
 Thr Ser Pro Ala Phe Ala Asn Arg Leu Pro His Ile Phe Lys Asp Pro
 385 390 395 400
 Asp Thr Tyr Asp Pro Glu Arg Phe Ser Pro Gly Arg Glu Glu Asp Lys
 405 410 415
 Ala Ala Gly Ala Phe Ser Tyr Ile Ala Phe Gly Gly Gly Arg His Gly
 420 425 430
 Cys Leu Gly Glu Pro Phe Ala Tyr Leu Gln Ile Lys Ala Ile Trp Ser
 435 440 445

His Leu Leu Arg Asn Phe Glu Leu Glu Leu Val Ser Pro Phe Pro Glu
 450 455 460

Ile Asp Trp Asn Ala Met Val Val Gly Val Lys Gly Asn Val Met Val
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Arg Tyr Lys Arg Arg Gln Leu Ser
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<210> 18
 <211> 1852
 <212> DNA
 <213> Arabidopsis thaliana

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 aagaagcgtc ttcctcttac tcttaaagct tggcctccat tggttggaag tcttatcaaa 360
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 aacgacatgc tgcagtgttt catcgaatca aagtacaaag atggtagaca gacaaccgaa 1020
 tctgaagtca ctggtttgct cattgctgct ctgtttgcag gacaacacac gagctctatc 1080
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atcttcaaag accccgacac ctacgaccca gaaagattct cccctggaag agaagaggac 1440
aaagccgcag gggcattctc gtacattgca ttcggagggg gaaggcacgg gtgccttgga 1500
gagccgtttg cttacctgca gatcaaagcc atatggagtc atttgttgag gaacttcgag 1560
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<210> 19
<211> 488
<212> PRT
<213> Arabidopsis thaliana

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<400> 19

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20           25           30
Asp Ser Lys Lys Lys Arg Leu Pro Pro Thr Leu Lys Ala Trp Pro Pro
35           40           45
Leu Val Gly Ser Leu Ile Lys Phe Leu Lys Gly Pro Ile Ile Met Leu
50           55           60
Arg Glu Glu Tyr Pro Lys Leu Gly Ser Val Phe Thr Val Asn Leu Val
65           70           75           80
His Lys Lys Ile Thr Phe Leu Ile Gly Pro Glu Val Ser Ala His Phe
85           90           95
Phe Lys Ala Ser Glu Ser Asp Leu Ser Gln Gln Glu Val Tyr Gln Phe
100          105          110
Asn Val Pro Thr Phe Gly Pro Gly Val Val Phe Asp Val Asp Tyr Ser
115          120          125
Val Arg Gln Glu Gln Phe Arg Phe Phe Thr Glu Ala Leu Arg Val Asn
130          135          140
Lys Leu Lys Gly Tyr Val Asp Met Met Val Thr Glu Ala Glu Asp Tyr
145          150          155          160

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Phe Ser Lys Trp Gly Glu Ser Gly Glu Val Asp Ile Lys Val Glu Leu
 165 170 175
 Glu Arg Leu Ile Ile Leu Thr Ala Ser Arg Cys Leu Leu Gly Arg Glu
 180 185 190
 Val Arg Asp Gln Leu Phe Asp Asp Val Ser Ala Leu Phe His Asp Leu
 195 200 205
 Asp Asn Gly Met Leu Pro Ile Ser Val Leu Phe Pro Tyr Leu Pro Ile
 210 215 220
 Pro Ala His Arg Arg Arg Asp Arg Ala Arg Glu Lys Leu Ser Glu Ile
 225 230 235 240
 Phe Ala Lys Ile Ile Gly Ser Arg Lys Arg Ser Gly Lys Thr Glu Asn
 245 250 255
 Asp Met Leu Gln Cys Phe Ile Glu Ser Lys Tyr Lys Asp Gly Arg Gln
 260 265 270
 Thr Thr Glu Ser Glu Val Thr Gly Leu Leu Ile Ala Ala Leu Phe Ala
 275 280 285
 Gly Gln His Thr Ser Ser Ile Thr Ser Thr Trp Thr Gly Ala Tyr Leu
 290 295 300
 Met Arg Tyr Lys Glu Tyr Phe Ser Ala Ala Leu Asp Glu Gln Lys Asn
 305 310 315 320
 Leu Ile Ala Lys His Gly Asp Lys Ile Asp His Asp Ile Leu Ser Glu
 325 330 335
 Met Asp Val Leu Tyr Arg Cys Ile Lys Glu Ala Leu Arg Leu His Pro
 340 345 350
 Pro Leu Ile Met Leu Met Arg Ala Ser His Ser Asp Phe Ser Val Thr
 355 360 365
 Ala Arg Asp Gly Lys Thr Tyr Asp Ile Pro Lys Gly His Ile Val Ala
 370 375 380
 Thr Ser Pro Ala Phe Ala Asn Arg Leu Pro His Ile Phe Lys Asp Pro
 385 390 395 400
 Asp Thr Tyr Asp Pro Glu Arg Phe Ser Pro Gly Arg Glu Glu Asp Lys
 405 410 415
 Ala Ala Gly Ala Phe Ser Tyr Ile Ala Phe Gly Gly Gly Arg His Gly
 420 425 430
 Cys Leu Gly Glu Pro Phe Ala Tyr Leu Gln Ile Lys Ala Ile Trp Ser
 435 440 445
 His Leu Leu Arg Asn Phe Glu Leu Glu Leu Val Ser Pro Phe Pro Glu
 450 455 460

Ile Asp Trp Asn Ala Met Val Val Gly Val Lys Gly Asn Val Met Val
 465 470 475 480

Arg Tyr Lys Arg Arg Gln Leu Ser
 485

<210> 20

<211> 1249

<212> DNA

<213> Arabidopsis thaliana

<400> 20

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tctgatctct ccggcggtc aatctccgca gaaaaagtca aagacaacta taaccaatac      180
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<210> 21

<211> 1444
 <212> DNA
 <213> *Nicotiana tabacum*

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 aagaataact atactgacat gggttaacaaa tactatgatc ttgacactag cttctacgaa 300
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<210> 22

<211> 1421

<212> DNA

<213> *Arabidopsis thaliana*

<400> 22

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gcagagcgta aaggcaaacg agccgtagat ctctctgggt gctcaatctc cgccgagaaa      180
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aagaaagctg gtctcgacgc gctttgcgag gtcgtgtgtg gtaacttcct ccagatgccg      600
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International Bureau



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(72) Inventors; and

(75) Inventors/Applicants (for US only): **KARUNANANDA, Balasulojini** [US/US]; c/o Monsanto Technology

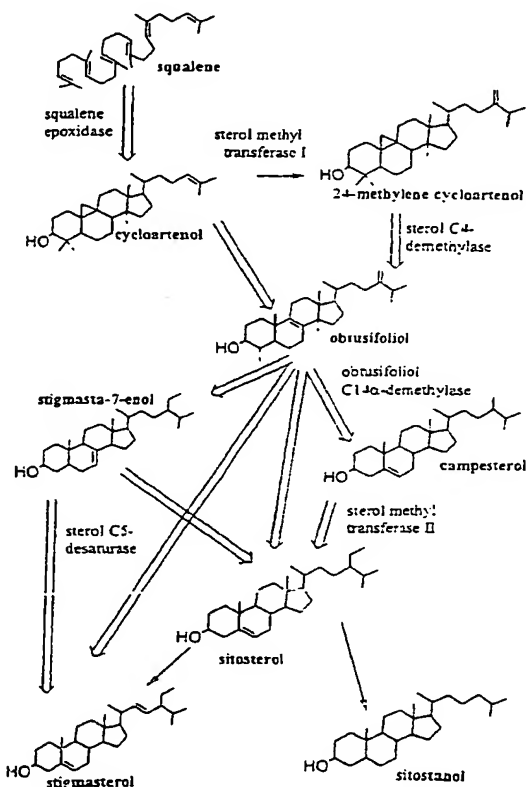
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(74) Agents: **MCBRIDE, Timothy, B.** et al.; Senniger, Powers, Leavitt & Roedel, One Metropolitan Square, 16th Floor, St. Louis, MO 63102 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,

[Continued on next page]

(54) Title: **TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROID COMPOUNDS**



(57) Abstract: Disclosed are constructs comprising sequences encoding 3-hydroxy-3methylglutaryl-Coenzyme A reductase and at least one other sterol synthesis pathway enzyme. Also disclosed are methods for using such constructs to alter sterol production and content in cells, plants, seeds and storage organs of plants. Also provided are oils and compositions containing altered sterol levels produced by use of the disclosed constructs. Novel nucleotide sequences useful in the alteration of sterol production are also provided. Also provided are cells, plants, seeds and storage organs of plants comprising sequences encoding 3-hydroxy-3methylglutaryl-Coenzyme A reductase, at least one other sterol synthesis pathway enzyme and at least one tocopherol synthesis enzyme.

WO 02/061072 A3



CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(BE, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

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(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent

(88) Date of publication of the international search report:
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INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US 02/00255

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 A01H5/00 C07K14/415 C12N15/82 C12N9/04 C12N9/02
C12N9/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, MEDLINE, EMBASE, SCISEARCH, CHEM ABS Data, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 00 61771 A (MONSANTO CO) 19 October 2000 (2000-10-19) page 11, line 19 - line 28 page 28, line 26 -page 29, line 16 page 30, line 19 - line 26 page 33, line 5 -page 37, line 28 page 101, line 10 - line 12 claims; example 5	1-54
Y	---	63-77
Y	WO 99 04622 A (UNIV NEVADA) 4 February 1999 (1999-02-04) the whole document ---	63-77
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☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

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A document defining the general state of the art which is not considered to be of particular relevance

E earlier document but published on or after the international filing date

L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

& document member of the same patent family

Date of the actual completion of the international search

26 June 2003

Date of mailing of the international search report

13.08.03

Name and mailing address of the ISA

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Burkhardt, P

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	SHINTANI DAVID ET AL: "Elevating the vitamin E content of plants through metabolic engineering." SCIENCE (WASHINGTON D C), vol. 282, no. 5396, 11 December 1998 (1998-12-11), pages 2098-2100, XP002245484 ISSN: 0036-8075 the whole document	63-77
Y	BACH T J ET AL: "CLONING OF CDNAS OR GENES ENCODING ENZYMES OF STEROL BIOSYNTHESIS FROM PLANTS AND OTHER EUKARYOTES: HETEROLOGOUS EXPRESSION AND COMPLEMENTATION ANALYSIS OF MUTATIONS FOR FUNCTIONAL CHARACTERIZATION" PROGRESS IN LIPID RESEARCH, PERGAMON PRESS, PARIS, FR, vol. 36, no. 2/3, September 1997 (1997-09), pages 197-226, XP000957903 ISSN: 0163-7827 cited in the application the whole document	1-54, 63-77
Y	SCHALLER H ET AL: "Overexpression of an Arabidopsis cDNA encoding a sterol-C24(1)-methyltransferase in tobacco modifies the ratio of 24-methyl cholesterol to sitosterol and is associated with growth reduction" PLANT PHYSIOLOGY, AMERICAN SOCIETY OF PLANT PHYSIOLOGISTS, ROCKVILLE, MD, US, vol. 118, no. 2, October 1998 (1998-10), pages 461-469, XP002130682 ISSN: 0032-0889 the whole document	1-54, 63-77
Y	SCHALLER HUBERT ET AL: "Expression of the Hevea brasiliensis (H.B.K.) Mull. Arg. 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 in tobacco results in sterol overproduction" PLANT PHYSIOLOGY, AMERICAN SOCIETY OF PLANT PHYSIOLOGISTS, ROCKVILLE, MD, US, vol. 109, no. 3, 1995, pages 761-770, XP002133624 ISSN: 0032-0889 cited in the application the whole document	1-54, 63-77

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 02/00255

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SCHAFER ULRIKE A ET AL: "An example of intron junctional sliding in the gene families encoding squalene monooxygenase homologues in Arabidopsis thaliana and Brassica napus." PLANT MOLECULAR BIOLOGY, vol. 39, no. 4, March 1999 (1999-03), pages 721-728, XP002245471 ISSN: 0167-4412 cited in the application the whole document	55,57-62
X	-& DATABASE EMBL 'Online! Arabidopsis thaliana Sqpl, 6 May 1998 (1998-05-06) "An example of intron junctional sliding in the gene families encoding squalene monooxygenase homologues in Arabidopsis thaliana and Brassica napus." retrieved from ENI Database accession no. AJ005930 XP002245573 abstract	55,57-62
X	--- DATABASE EMBL 'Online! Arabidopsis thaliana cDNA clone, 9 April 2000 (2000-04-09) NAKAMURA AND ASAMI: "A large scale analysis of cDNA in Arabidopsis thaliana: generation of 12,028 non-redundant expressed sequence tags from normalized size-selected cDNA libraries." retrieved from EBI Database accession no. AV440215 XP002245474 abstract --- -/--	55,57-62

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 02/00255

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	CABELLO-HURTADO FRANCISCO ET AL: "Cloning and functional expression in yeast of a cDNA coding for an obtusifolios 14-alpha-demethylase (CYP51) in wheat." BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 230, no. 2, 1997, pages 381-385, XP002245472 ISSN: 0006-291X the whole document	56-62
X	-& DATABASE EMBL 'Online! T. aestivum mRNA, 4 December 1996 (1996-12-04) CABELLO-HURTADO ET AL.: "Cloning and functional expression in yeast of a cDNA coding for an obtusifolios 14-alpha-demethylase (CYP51) in wheat." retrieved from EBI Database accession no. Y09291 XP002245574 abstract	56-62
X	--- BAK SOREN ET AL: "Cloning and expression in Escherichia coli of the obtusifolios 14-alpha-demethylase of Sorghum bicolor (L.) Moench, a cytochrome P450 orthologous to the sterol 14-alpha-demethylases (CYP51) from fungi and mammals." PLANT JOURNAL, vol. 11, no. 2, 1997, pages 191-201, XP002245473 ISSN: 0960-7412 cited in the application the whole document	56-62
X	-& DATABASE EMBL 'Online! Sorghum bicolor mRNA, 19 November 1996 (1996-11-19) BAK ET AL.: "Cloning and expression in Escherichia coli of the obtusifolios 14-alpha-demethylase of Sorghum bicolor (L.) Moench, a cytochrome P450 orthologous to the sterol 14-alpha-demethylases (CYP51) from fungi and mammals." retrieved from EBI Database accession no. U74319 XP002245575 abstract	56-62
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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 02/00255

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL 'Online! Lotus japonicus nodule library, mRNA sequence, 21 April 2000 (2000-04-21) COLEBATCH ET AL.: "Lotus japonicus root nodule ESTs: tools for functional genomics" retrieved from EBI Database accession no. AW719774 XP002245475 abstract</p> <p>---</p>	56-62
X	<p>DATABASE EMBL 'Online! Tomato radicle, 5 d post-imbibition, 29 May 2000 (2000-05-29) VAN DER HOEVEN ET AL.: "Generation of ESTs from tomato radicle tissue (etiolated)" retrieved from EBI Database accession no. AW625933 XP002245476 abstract</p> <p>---</p>	56-62
A	<p>NGUYEN TU T: "The cholesterol-lowering action of plant stanol esters." JOURNAL OF NUTRITION, vol. 129, no. 12, December 1999 (1999-12), pages 2109-2112, XP002236376 ISSN: 0022-3166 the whole document</p> <p>---</p>	1-54, 63-77
A	<p>JENKINS D J ET AL: "Plant sterols, health claims and strategies to reduce cardiovascular disease risk." JOURNAL OF THE AMERICAN COLLEGE OF NUTRITION. UNITED STATES DEC 1999, vol. 18, no. 6, December 1999 (1999-12), pages 559-562, XP002236377 ISSN: 0731-5724 the whole document</p> <p>-----</p>	1-54, 63-77

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1 - 54, 63 - 68

relating to a method of increasing the formation of steroid pathway products by transforming host cells with DNA constructs or vectors containing DNA sequences encoding a 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGR) and a so-called steroid pathway enzyme; cells, plant parts and whole plants resulting from said method and oils extracted from said plant parts.

2. Claims: 55 (completely), 57 - 62 (all partially)

relating to SEQ ID NOs:4,6,8 an Arabidopsis squalene epoxidase, constructs, vectors and host cells containing said SEQ ID NOs and methods of producing said squalene epoxidase by culturing said host cells.

3. Claims: 56 (completely), 57 - 62 (all partially)

relating to SEQ ID NOs:12,14,17 an Arabidopsis obtusifolius C14-alpha demethylase, constructs, vectors and host cells containing said SEQ ID NOs and methods of producing said obtusifolius C14-alpha demethylase by culturing said host cells.

4. Claims: 69 - 77

relating to a method of increasing steroid pathway products and tocopherols by transforming host cells with vectors containing DNA sequences encoding a HMGR, a so-called steroid pathway enzyme and a so-called tocopherol synthesis pathway enzyme; plants resulting from said method and oil extracted from the seeds of said plants.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 02/00255

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Although claims 52 and 53 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☒ Claims Nos.: 56 - 62 (all partially)
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 56 - 62 (all partially)

Present claim 56 refers to an isolated nucleotide sequence selected from SEQ ID NOs:12, 14 or 17. SEQ ID NO:17, however, refers to an amino acid sequence. The search has therefore been limited to SEQ ID NOs:12 and 14 that refer to nucleic acid sequences.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT
Information on patent family members

International Application No

PCT/US 02/00255

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 0061771	A	19-10-2000	AU 4231600 A	14-11-2000
			BR 0010597 A	13-02-2002
			CA 2372120 A1	19-10-2000
			CN 1360637 T	24-07-2002
			EP 1169462 A2	09-01-2002
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WO 9904622	A	04-02-1999	AU 8506198 A	16-02-1999
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